

REPLACEMENT SHEET

1 ATGGATTTTC TCCTGGCGCT GGTGCTGGTA TCCTCGCTCT ACCTGCAGGC
51 GGCCGCCGAG TTCGACGGGA GGTGGCCAG GCAAATAGTG TCATCGATTG
101 GCCTATGTCG TTATGGTGGG AGGATTGACT GCTGCTGGGG CTGGGCTCGC
151 CAGTCTTGGG GACAGTGTCA GCCTTTCTAC GTCTTAAGGC AGAGAATAGC
201 CAGGATAAGG TGCCAGCTCA AAGCTGTGTG CCAACCACGA TGCAAACATG
251 GTGAATGTAT CGGGCCAAAC AAGTGCAAGT GTCATCCTGG TTATGCTGGA
301 AAAACCTGTA ATCAAGACGA GCACATCCCA GCTCCTCTTG ACCAAGGCAG
351 TGAACAGCCT CTTTTCCAAC CCCTGGATCA CCAAGCCACA AGTTTGCCTT
401 CAAGGGATCT AAATGAGTGT GGCCTGAAGC CCCGGCCCTG TAAGCACAGG
451 TGCATGAACA CTTACGGCAG CTACAAGTGC TACTGTCTCA ACGGATATAT
501 GCTCATGCCG GATGGTTCTT GCTCAAGTGC CCTGACCTGC TCCATGGCAA
551 ACTGTCAGTA TGGCTGTGAT GTTGTTAAAG GACAAATACG GTGCCAGTGC
601 CCATCCCCTG GCCTGCAGCT GGCTCCTGAT GGGAGGACCT GTGTAGATGT
651 TGATGAATGT GCTACAGGAA GAGCCTCCTG CCCTAGATTT AGGCAATGTG
701 TCAACACTTT TGGGAGCTAC ATCTGCAAGT GTCATAAAGC CTTCGATCTC
751 ATGTATATTG GAGGCAAATA TCAATGTCAT GACATAGACG AATGCTCACT
801 TGGTCAGTAT CAGTGCAGCA GCTTTGCTCG ATGTTATAAC GTACGTGGGT
851 CCTACAAGTG CAAATGTAAA GAAGGATACC AGGGTGATGG ACTGACTTGT
901 GTGTATATCC CAAAAGTTAT GATTGAACCT TCAGGTCCAA TTCATGTACC
951 AAAGGGAAAT GGTACCATTT TAAAGGGTGA CACAGGAAAT AATAATTGGA
1001 TTCCTGATGT TGGAAGTACT TGGTGGCCTC CGAAGACACC ATATATTCCT
1051 CCTATCATTA CCAACAGGCC TACTTCTAAG CCAACAACAA GACCTACACC
1101 AAAGCCAACA CCAATTCTTA CTCCACCACC ACCACCACCC CTGCCAACAG
1151 AGCTCAGAAC ACCTCTACCA CCTACAACCC CAGAAAGGCC AACCACCGGA
1201 CTGACAACTA TAGCACCAGC TGCCAGTACA CCTCCAGGAG GGATTACAGT
1251 TGACAACAGG GTACAGACAG ACCCTCAGAA ACCCAGAGGA GATGTGTTCA
1301 TTCCACGGCA ACCTTCAAAT GACTTGTTTG AAATATTTGA AATAGAAAGA
1351 GGAGTCAGTG CAGACGATGA AGCAAAGGAT GATCCAGGTG TTCTGGTACA
1401 CAGTTGTAAT TTTGACCATG GACTTTGTGG ATGGATCAGG GAGAAAGACA
1451 ATGACTTGCA CTGGGAACCA ATCAGGGACC CAGCAGGTGG ACAATATCTG
1501 ACAGTGTCCG CAGCCAAAGC CCCAGGGGGA AAAGCTGCAC GCTTGGTGCT
1551 ACCTCTCGGC CGCCTCATGC ATTGAGGGGA CCTGTGCCCTG TCATTCAGGC
1601 ACAAGGTGAC GGGGCTGCAC TCTGGCACAC TCCAGGTGTT TGTGAGAAAA
1651 CACGGTGCCC ACGGAGCAGC CCTGTGGGGA AGAAATGGTG GCCATGGCTG
1701 GAGGCAAACA CAGATCACCT TGCGAGGGG TGACATCAAG AGCGTCGTCT
1751 TCAAAGGTGA AAAAAGGCGT GGTCACTG GGGAGATTGG ATTAGATGAT
1801 GTGAGCTTGA AAAAAGGCCA CTGCTCTGAA GAACGCTAA (SEQ ID NO:1)

FEATURES:

Start Codon: 1
Stop Codon: 1837

Homologous proteins:

Top 10 BLAST Hits:

				Score	E
CRA	50000098943299	/altid=gi 15795193	/def=ref NP_277060.1 nep...	1190	0.0
CRA	46000103872918	/altid=gi 15128103	/def=gb AAK84391.1 AF3970...	1147	0.0
CRA	84000042916333	/altid=gi 15430248	/def=gb AAK96011.1 (AY03...	1128	0.0
CRA	84000042916331	/altid=gi 15430246	/def=gb AAK96010.1 (AY03...	1084	0.0
CRA	78000201656899	/altid=gi 14763663	/def=ref XP_040394.1 epi...	397	e-109
CRA	163000000492958	/altid=gi 9506563	/def=ref NP_062270.1 EGF...	396	e-109
CRA	157000140328010	/altid=gi 6752658	/def=gb AAF27812.1 AF1860...	396	e-109
CRA	157000140333453	/altid=gi 13124888	/def=ref NP_056322.2 ep...	395	e-109
CRA	1000682328934	/altid=gi 7512796	/def=pir T17324 hypothetical...	385	e-106
CRA	60000046724650	/altid=gi 13929180	/def=ref NP_114014.1 fib...	147	4e-34

FIGURE 1A



REPLACEMENT SHEET

Blast hits to dbEST:

<u>CRA Number</u>	<u>gi Number</u>	<u>Score</u>	<u>Expect</u>
CRA 113000119195127	gi 14391046	1068 bits (539)	0.0
CRA 110000024586745	gi 12320908	866 bits (437)	0.0
CRA 87000000737360	gi 7312275	842 bits (425)	0.0
CRA 113000119269070	gi 14399233	831 bits (419)	0.0
CRA 113000119283425	gi 14400823	827 bits (417)	0.0
CRA 113000119283416	gi 14400822	785 bits (396)	0.0
CRA 112000057002060	gi 14377756	680 bits (343)	0.0
CRA 147000029699826	gi 11300389	668 bits (337)	0.0
CRA 117000088322182	gi 12462132	563 bits (284)	1e-157

Expression (Tissue Source):

<u>gi Number</u>	<u>Organ</u>
gi 14391046	head_neck
gi 12320908	nervous_tumor
gi 7312275	head_neck
gi 14399233	head_neck
gi 14400823	head_neck
gi 14400822	head_neck
gi 14377756	colon
gi 11300389	breast_normal
gi 12462132	placenta_normal

FIGURE 1B



REPLACEMENT SHEET

1 MDFLLALVLV SSLYLQAAAE FDGRWPRQIV SSIGLCRYGG RIDCCWGWAR
51 QSWGQCQPFY VLRQRIARIR CQLKAVCQPR CKHGECIGPN KCKCHPGYAG
101 KTCNQDEHIP APLDQGSEQP LFQPLDHQAT SLPSRDLNEC GLKPRPCKHR
151 CMNTYGSYKC YCLNGYMLMP DGSCSSALTC SMANCQYGCD VVKGQIRCQC
201 PSPGLQLAPD GRTCVDVDEC ATGRASCPRF RQCVNTFGSY ICKCHKGFDL
251 MYIGGKYQCH DIDECSLGQY QCSSFARCYN VRGSYKCKCK EGYQGDGLTC
301 VYIPKVMIEP SGPIHVPKGN GTILKGDGTGN NNWIPDVGST WWPPKTPYIP
351 PIITNRPTSK PTTTRPTPKPT PIPTPPPPPP LPTELRTPLP PTTPERPTTG
401 LTTIAPAAST PPGGITVDNR VQTDPOKPRG DVFIPRQPSN DLFEIFEIER
451 GVSADDEAKD DPGVLVHSCN FDHGLCGWIR EKDNLDHWEP IRDPAGGQYL
501 TVSAAKAPGG KAARLVLPLG RLMHSGDLCL SFRHKVTGLH SGTQLQVFVRK
551 HGAHGAALWG RGGHGWQRQT QITLRGADIK SVVFKGEKRR GHTGEIGLDD
601 VSLKKGHCSE ER (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

Prosite results:

PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

320-323 NGTI (residues 320-323 of SEQ ID NO:2)

PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 10

1	157-159	SYK
2	222-224	TGR
3	284-286	SYK
4	354-356	TNR
5	358-360	TSK
6	362-364	TTR
7	366-368	TPK
8	531-533	SFR
9	573-575	TLR
10	602-604	SLK

PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 3

1	213-216	TCVD (residues 213-216 of SEQ ID NO:2)
2	392-395	TTPE (residues 392-395 of SEQ ID NO:2)
3	453-456	SADD (residues 453-456 of SEQ ID NO:2)

PDOC00007 PS00007 TYR_PHOSPHO_SITE

Tyrosine kinase phosphorylation site

246-252 KGFDLMY (residues 246-252 of SEQ ID NO:2)

PDOC00008 PS00008 MYRISTYL

N-myristoylation site

Number of matches: 10

1	156-161	GSYKCY (residues 156-161 of SEQ ID NO:2)
2	172-177	GSCSSA (residues 172-177 of SEQ ID NO:2)
3	194-199	GQIRCQ (residues 194-199 of SEQ ID NO:2)
4	238-243	GSYICK (residues 238-243 of SEQ ID NO:2)
5	268-273	GQYQCS (residues 268-273 of SEQ ID NO:2)
6	283-288	GSYKCK (residues 283-288 of SEQ ID NO:2)
7	497-502	GQYLTV (residues 497-502 of SEQ ID NO:2)
8	509-514	GGKAAR (residues 509-514 of SEQ ID NO:2)
9	538-543	GLHSGT (residues 538-543 of SEQ ID NO:2)
10	552-557	GAHGAA (residues 552-557 of SEQ ID NO:2)

FIGURE 2A



REPLACEMENT SHEET

PDOC00010 PS00010 ASX_HYDROXYL

Aspartic acid and asparagine hydroxylation site

Number of matches: 3

1	151-162	CMNTYGSYKCYC	(residues 151-162 of SEQ ID NO:2)
2	233-244	CVNTFGSYICKC	(residues 233-244 of SEQ ID NO:2)
3	278-289	CYNVRGSYKCKC	(residues 278-289 of SEQ ID NO:2)

PDOC00016 PS00016 RGD

Cell attachment sequence

429-431 RGD

PDOC00021 PS00022 EGF_1

EGF-like domain signature 1

92-103 CKCHPGYAGKTC (residues 92-103 of SEQ ID NO:2)

PDOC00021 PS01186 EGF_2

EGF-like domain signature 2

Number of matches: 3

1	92-103	CKCHPGYAGKTC	(residues 92-103 of SEQ ID NO:2)
2	160-174	CYCLNGYMLMPDGSC	(residues 160-174 of SEQ ID NO:2)
3	287-300	CKCKEGYQGDGLTC	(residues 287-300 of SEQ ID NO:2)

PDOC00913 PS01187 EGF_CA

Calcium-binding EGF-like domain signature

Number of matches: 3

1	136-160	DLNECGLKPRPCKHRCMNTYGSYKC	(res. 136-160 of SEQ ID NO:2)
2	216-242	DVDECATGRASCPFRQCVNTFGSYIC	(res. 216-242 of SEQ ID NO:2)
3	261-287	DIDECSLGQYQCSSFARCYNVRGSYKC	(res. 261-287 of SEQ ID NO:2)

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	3	23	0.942	Putative
2	163	183	0.765	Putative
3	397	417	1.209	Certain

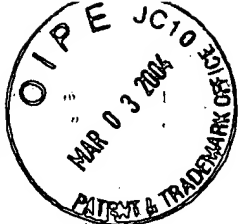
SignalP results:

< Is the sequence a signal peptide?

#	Measure	Position	Value	Cutoff	Conclusion
	max. C	20	0.657	0.37	YES
	max. Y	20	0.713	0.34	YES
	max. S	6	0.960	0.88	YES
	mean S	1-19	0.901	0.48	YES

Most likely cleavage site between pos. 19 and 20: AAA-EF

FIGURE 2B



REPLACEMENT SHEET

BLAST Alignment to Top Hit:

>CRA|50000098943299 /altid=gi|15795193 /def=ref|NP_277060.1|
nephronectin [Mus musculus] /org=Mus musculus
/taxon=10090 /div=ROD /dataset=nraa /length=609
Length = 609

Score = 1190 bits (3045), Expect = 0.0

Identities = 536/610 (87%), Positives = 569/610 (92%), Gaps = 3/610 (0%)

Query: 1 MDPLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
M LLA VL SLYLQ AA+FDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY
Sbjct: 1 MAVLLAAVLASSLYLQVAADFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60

Query: 61 VLRQRIARIRCQLKAVCQPRCKHGECIGPNKCKCHPGYAGKTCNQDEHI-PAPLDQGSEQ 119
VLRQR+ARIRCQLKAVCQP+CKHGEC+GPNKCKCHPG+AGKTCNQDE P PLDQGSEQ
Sbjct: 61 VLRQLLARIRCQLKAVCQPQCKHGECVGPKNCKCHPGFAGKTCNQDESFHPTPLDQGSEQ 120

Query: 120 PLFQPLDHQATSLPSRDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGSCSSALT 179
PLFQP DHQAT++PSRDLNECGLKPRPCKHRCMNT+GSYKCYCLNGYML+PDGSCSSAL+
Sbjct: 121 PLFQPPDHQATNVPSRDLNECGLKPRPCKHRCMNTFGSYKCYCLNGYMLLPDGSCSSALS 180

Query: 180 CSMANCQYGCDVVKGQIRCQCPSPGLQLAPDGRTCVDVDECATGRASCPRFRQCVNTFGS 239
CSMANCQYGCDVVKGQ+RCQCPSPGLQLAPDGRTCVD+DECATGR SCPRFRQCVNTFGS
Sbjct: 181 CSMANCQYGCDVVKGQVRCQCPSPGLQLAPDGRTCVDIDECATGRVSCPRFRQCVNTFGS 240

Query: 240 YICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLT 299
YICKCH GFDLMYIGGKYQCHDIDECSLGQ+QCSS+ARCYN+ GSYKC+C++GY+GDGL
Sbjct: 241 YICKCHTGFDLMYIGGKYQCHDIDECSLGQHQCSSYARCYNIHGSYKCQCRDGYEGDGLN 300

Query: 300 CVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNNWIPDVGSTWWPPKTPYIPPIITNRPTS 359
CVYIPKVMIEPSGPIH+P+ NGTI KGD G+ N IPD GST WP KTPYIPP+ITNRPTS
Sbjct: 301 CVYIPKVMIEPSGPIHMPERNGTISKGDGGHANRIPDAGSTRWPLKTPYIPPVITNRPTS 360

Query: 360 KPTRPTPKPTPIPTPPPPPLTELRT-PLPPTPERPTTGLTTIAPAASTPPGGITVD 418
KPTRPTP PTP PTPPPPPPLTE RT PLPPT PERP+T TTIAPA ST ITVD
Sbjct: 361 KPTRPTPNPTPQPTPPPPPLTEPRTTLPPT-PERPSTRPTTIAPATSTTTTRVITVD 419

Query: 419 NRVTQDPQKPRGDVFI PRQPSNDLFEIFEIERGVSADDEAKDDPGVLVHSCNFDHGLCGW 478
NR+QTDPQKPRGDVFI PRQP+NDLFEIFEIERGVSAD+E KDDPG+L+HSCNFDHGLCGW
Sbjct: 420 NRIQTDPQKPRGDVFI PRQPTNDLFEIFEIERGVSADDEEVKDDPGILHSCNFDHGLCGW 479

Query: 479 IREKDNLDHWEPIRDPAGGQYLTVSAAKAPGGKAARLVLPGLRLMHSGDLCLSFRHKVTG 538
IREKD+DLHWE RDPAGGQYLTVSAAKAPGGKAARLVL LG LMHSGDLCLSFRHKVTG
Sbjct: 480 IREKSDLDHWETARDPAGGQYLTVSAAKAPGGKAARLVRLGHLMHSGDLCLSFRHKVTG 539

Query: 539 LHSGLTQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSVVFKGEKRRGHTGEIGL 598
LHSGLTQVFVRKHG HGAALWGRNGGHGWRQTQITLRGAD+KSV+FKGEKRRGHTGEIGL
Sbjct: 540 LHSGLTQVFVRKHGTHGAALWGRNGGHGWRQTQITLRGADVKSIVFKGEKRRGHTGEIGL 599

Query: 599 DDVSLKKGHC 608
DDVSLK+G C
Sbjct: 600 DDVSLKRGRC 609 (SEQ ID NO:4)

FIGURE 2C



REPLACEMENT SHEET

>CRA|46000103872918 /altid=gi|15128103 /def=gb|AAK84391.1|AF397007_1
(AF397007) nephronectin [Mus musculus] /org=Mus musculus
/taxon=10090 /div=ROD /dataset=nraa /length=592
Length = 592

Score = 1147 bits (2934), Expect = 0.0

Identities = 520/610 (85%), Positives = 552/610 (90%), Gaps = 20/610 (3%)

Query: 1 MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
M LLA VL SLYLQ AA+FDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQ
Sbjct: 1 MAVLLAAVLASSLYLQVAADFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQ-- 58

Query: 61 VLRQRIARIRCQLKAVCQPRCKHGEICGPNKCKCHPGYAGKTCNQDEHI-PAPLDQGSEQ 119
VCQP+CKHGEIC+GPNKCKCHPG+AGKTCNQDE P PLDQGSEQ
Sbjct: 59 -----VCQPQCKHGEICVGPKNCKCHPGFAGKTCNQDES FHTPLDQGSEQ 103

Query: 120 PLFQPLDHQATSLPSRDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGCSSSALT 179
PLFQP DHQAT++PSRDLNECGLKPRPCKHRCMNT+GSYKCYCLNGYML+PDGCSSSAL+
Sbjct: 104 PLFQPPDHQATNVPSRDLNECGLKPRPCKHRCMNTFGSYKCYCLNGYMLLPDGCSSSALS 163

Query: 180 CSMANCQYGC DVVKGQIRQCQPSGLQLAPDGRTCVDVDECATGRASCPFRQC VNTFGS 239
CSMANCQYGC DVVKGQ+RCQCQPSGLQLAPDGRTCVD+DECATGR SCPRFRQC VNTFGS
Sbjct: 164 CSMANCQYGC DVVKGQVRCQCQPSGLQLAPDGRTCVDIDEATGRVSCPRFRQC VNTFGS 223

Query: 240 YICKCHKGF DLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLT 299
YICKCH GFDLMYIGGKYQCHDIDECSLGQ+QCSS+ARCYN+ GSYKC+C++GY+GDGL
Sbjct: 224 YICKCHTGFDLMYIGGKYQCHDIDECSLGQHQCSSYARCYNIHGSYKCQCRDGYEGDGLN 283

Query: 300 CVYIPKVMIEPSGPIHVPKNGTILKGD TGNNWIPDVGSTWWPPKTPYIPPIITNRPTS 359
CVYIPKVMIEPSGPIH+P+ NGTI KGD G+ N IPD GST WP KTPYIPP+ITNRPTS
Sbjct: 284 CVYIPKVMIEPSGPIHMPERNGTISKGDGGHANRIPDAGSTRWPLKTPYIPPVITNRPTS 343

Query: 360 KPTRPTPKPTPIPTPPPPPLTELRT-PLPPTPERPTTGLTTIAPAASTPPGGITVD 418
KPTRPTP PTP PTPPPPPPLTE RT PLPPT PERP+T TTIAPA ST ITVD
Sbjct: 344 KPTRPTPNPTPQPTPPPPPLTEPRTTPLPPT-PERPSTRPTTIAPATSTTTTRVITVD 402

Query: 419 NRVTQDPQKPRGDVFIPRQPSNDLFEIFEIERGVSADDEAKDDPGVLVHSCNFDHGLCGW 478
NR+QTDPQKPRGDVFIPRQP+NDLFEIFEIERGVSAD+E KDDPG+L+HSCNFDHGLCGW
Sbjct: 403 NRIQTDPQKPRGDVFIPRQPTNDLFEIFEIERGVSADDEEVKDDPGILHSCNFDHGLCGW 462

Query: 479 IREKNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVLPLGRLMHSGDLCLSFRHKVTG 538
IREKD+DLHWE RDPAGGQYLTVSAAKAPGGKAARLVL LG LMHSGDLCLSFRHKVTG
Sbjct: 463 IREKSDLHWETARDPAGGQYLTVSAAKAPGGKAARLVLRLGHLMHSGDLCLSFRHKVTG 522

Query: 539 LHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSVVFKGEKRRGHTGEIGL 598
LHSGTLQVFVRKHG HGAALWGRNGGHGWRQTQITLRGAD+KSV+FKGEKRRGHTGEIGL
Sbjct: 523 LHSGTLQVFVRKHGTHGAALWGRNGGHGWRQTQITLRGADVKS VIFKGEKRRGHTGEIGL 582

Query: 599 DDVSLKKGHC 608
DDVSLK+G C
Sbjct: 583 DDVSLKRGRC 592 (SEQ ID NO:5)

FIGURE 2D



REPLACEMENT SHEET

>CRA|84000042916333 /altid=gi|15430248 /def=gb|AAK96011.1|
 (AY035899) nephronectin long isoform [Mus musculus]
 /org=Mus musculus /taxon=10090 /div=ROD /dataset=nraa
 /length=578
 Length = 578

Score = 1128 bits (2885), Expect = 0.0
Identities = 512/609 (84%), Positives = 543/609 (89%), Gaps = 32/609 (5%)

Query: 1 MDLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
 M LLA VL SLYLQ AA+FDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY
Sbjct: 1 MAVLLAAVLASSLYLQVAADFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60

Query: 61 VLRQRIARIRCQLKAVCQPRCKHGECIGPNKCKCHPGYAGKTCNQDEHIPAPLDQGSEQP 120
 VLRQR+ARIRCQLKAVCQP+CKHGEC+GPNKCKCHPG+AGKTCNQ
Sbjct: 61 VLRQLARIRCQLKAVCQPQCKHGECVGNKCKCHPGFAGKTCNQ----- 105

Query: 121 LFQPLDHQATSLPSRDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGSCSSALTC 180
 DLNECGLKPRPCKHRCMNT+GSYKCYCLNGYML+PDGSCSSAL+C
Sbjct: 106 -----DLNECGLKPRPCKHRCMNTFGSYKCYCLNGYMLLPDGSCSSALSC 150

Query: 181 SMANCQYGC DVVKGQIRCQCPSGLQLAPDGRTCVDVDECATGRASCPFRQC VNTFGSY 240
 SMANCQYGC DVVKGQ+RCQCPSGLQLAPDGRTCVD+DECATGR SCPRFRQC VNTFGSY
Sbjct: 151 SMANCQYGC DVVKGQVRCQCPSGLQLAPDGRTCVDIDECATGRVSCPRFRQC VNTFGSY 210

Query: 241 ICKCHKGF DLMYIGGKYQCHDIDEC SLGQYQC SSFARCYNVRGSYKCKCKEGYQGDGLTC 300
 ICKCH GFDLMYIGGKYQCHDIDEC SLGQ+QCSS+ARCYN+ GSYKC+C++GY+GDGL C
Sbjct: 211 ICKCHTGFDLMYIGGKYQCHDIDEC SLGQHQC SSYARCYNIHGSYKQCQCRDGYEGDGLNC 270

Query: 301 VYIPKVMIEPSGPIHVPKNGNTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRPTSK 360
 VYIPKVMIEPSGPIH+P+ NGTI KGD G+ N IPD GST WP KTPYIPP+ITNRPTSK
Sbjct: 271 VYIPKVMIEPSGPIHMPERNGTISKGDGGHANRIPDAGSTRWPLKTPYIPPVITNRPTSK 330

Query: 361 PTTRPTPKPTPIPTPPPPPLPTEL R-TPLPPTTPTTGLTTIAPAASTPPGGITVDN 419
 PTTRPTP PTP PTPPPPPPLPTE R TPLPP TPERP+T TTIAPA ST ITVDN
Sbjct: 331 PTTRPTPNPTPQPTPPPPPLPTEPRTTPLPP-TPERPSTRPTTIAPATSTTTTRVITVDN 389

Query: 420 RVQTD PQKPRGDVFIPRQPSNDLFEIFEIERGVSADDEAKDDPGVLVHSCNFDHGLCGWI 479
 R+QTD PQKPRGDVFIPRQP+NDLFEIFEIERGVSAD+E KDDPG+L+HSCNFDHGLCGWI
Sbjct: 390 RIQTD PQKPRGDVFIPRQPTNDLFEIFEIERGVSADDEEVKDDPGILIHSCNFDHGLCGWI 449

Query: 480 REKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLV LPLGRLMHSGDLCLSF RHKVTGL 539
 REKD+DLHWE RDPAGGQYLTVSAAKAPGGKAARLV LG LMHSGDLCLSF RHKVTGL
Sbjct: 450 REKSD LHWETARDPAGGQYLTVSAAKAPGGKAARLV LRLGRLMHSGDLCLSF RHKVTGL 509

Query: 540 HSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSVVFKGEKRRGHTGEIGLD 599
 HSGTLQVFVRKHG HGAALWGRNGGHGWRQTQITLRGAD+KSV+FKGEKRRGHTGEIGLD
Sbjct: 510 HSGTLQVFVRKHGTHGAALWGRNGGHGWRQTQITLRGADVKSIVFKGEKRRGHTGEIGLD 569

Query: 600 DVSLKKGHC 608
 DVSLK+G C
Sbjct: 570 DVSLKRGRC 578 (SEQ ID NO:6)

FIGURE 2E



REPLACEMENT SHEET

Hmmer search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
CE00409	E00409 fibulin	108.3	3.8e-30	3
PF00629	MAM domain.	88.2	1.7e-22	1
PF00008	EGF-like domain	68.0	1.7e-17	5
CE00283	E00283 selectin	13.0	0.014	2
PF01278	Omptin family	1.9	6.6	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00008	1/5	77	103 ..	1	45 []	17.3	0.0036
CE00283	1/2	74	105 ..	119	153 ..	10.7	0.059
PF00008	2/5	140	172 ..	1	42 []	19.4	0.00091
PF00008	3/5	180	214 ..	1	45 []	19.0	0.0012
CE00409	1/3	136	227 ..	415	514 ..	69.4	4.5e-19
CE00283	2/2	226	248 ..	124	146 ..	8.7	0.2
PF00008	4/5	220	249 ..	1	41 []	10.8	0.25
CE00409	2/3	232	273 ..	429	473 ..	35.2	2.3e-09
CE00409	3/3	277	298 ..	344	365 ..	16.3	0.00053
PF00008	5/5	265	300 ..	1	45 []	31.7	2.9e-07
PF01278	1/1	477	493 ..	241	257 ..	1.9	6.6
PF00629	1/1	469	610 ..	1	170 []	88.2	1.7e-22

FIGURE 2F



REPLACEMENT SHEET

1 GAGAAAATTG AGATTACTAC CTGCAAGGTG TCATTACCTG GTAAGAAGCC
51 TATCAAAAAGT TTGTCCTCCT GAAAAAGTAG TTATTGCTAA AAGCTAGCTG
101 TTTTGATCTC ATTCTTGCTC ATTTGTTTTT AAGACTGAGA TAATGAAATG
151 TCACTCCCAT GGCAACTCTG CCTCTTTTTT GGAATGATCA TTGGTGGTCA
201 TAGTTGCAGC ATAATAACCA GTTAGACCTT GGAAATCCTT TAGATTCTCC
251 TTATTCCATG ATTTAACAAA GACTGATATA ATTAGCTACA TTTTACTGAA
301 GGGAGAAGCT AAAGTTCACA GGCAGAATTC AATTTAATCC AATCCATCTG
351 TTTNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 CTAATGTCTC ACGGGACCCA GAGTGGTAGG GAGGCAATGA CAACACAATA
501 CATTAAAGAGC TACCTTAGAG CATGCTAAGT GTAATAGAAG TATATAAAAC
551 ACTAGTCTCA GCCAATCAAA AAGTCAGAAA AGGCTTCCTG GGGGACTGTC
601 GGCTAAATTT AAACTCAAAG GGTAAGGGGA GATTGTCCAA ATGAAGAAGG
651 AAGAGGAATG AAGAGGAGGC TAAATTTAAA TGAAGAAGGA GTGTTTTCTA
701 GGCCAAAGCA AATATATGGA AAACAAAAGA AAGACGCATG TAGATGGGGC
751 ATTACACTTT TCCCTCCAGT TATTTATCCT GTTTTCATCC ACCACTCTTC
801 GTCTTTTCCT TAGATCTCCA GTTTTTTAGC CGTATATTAC CCCCTTTCTC
851 TCTAATCATC CATTGCACAC AGTGAGGTTT ATTTGTAAAT CTAACCCAGG
901 CACCAACTAA CCAACCAACA AACAAAAACA GCTAAGGAGT AGCCACTGGA
951 ACCTGGAACC ATGCCTACAC TTACAAAAAT TTGATTTTCT GCAGAAAAAA
1001 TATTTTGACT CCTACATTTT TGGACTTCAT TAGAAGGACC TGAAATGGAT
1051 GACACCAAGC TGTTTGCGTA AAATAATGTC CCAAGCCTGA ATTGGCATGG
1101 ATCTTTCTTG AGATTAAAAT AGAAACTTGT TTTGCTAACT GAAAACAACT
1151 TAGAAATCAA AGAGCCATTT AAGTTGAAAC CATTATTTTT CTTTCCTTG
1201 AAGAAAATTC CTGTTTTCAC ACACACTGAA TGATCAGGAT AGTGAATCAC
1251 CCTACCACAG AACTTTCCAT TAAAAATTTG AAGTTGTAGA AACCTCAAAA
1301 AGAAAATGAA GATGGGGGGA AAACGTTTGT AATGTAGCAA ATGANNNNNN
1351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNAGATG ATCACTGCAC
1901 AAGGCTGTCA TTCGAGGTAA GGTTGGGAAG AGGGGTGACT TGATTGGGCT
1951 CATGTACATC TTAGGATAAT CATGTTTTCA TTTGAACACA GTCATTTAGT
2001 ACAATACTTT TTACTCTGCA ACAACTGAAC AATGATTACT TAAAATGGTT
2051 TCTAAGTGAT CCCCTCAAGA TCAGGCACCA CAACACTACT AGGCAGTAGC
2101 AGCCCTTCCT CTCTGGCAGG CACTCATCCC TAGAGGGGCA GTCCTGTCCT
2151 AATGTGCTCG GGAGTTGAGC TGATAGAGAC AGAAACAGTC TGCTCATTTT
2201 TTCTTCAAAA CCCGACTGGA GAGCCAAATA TTTCTTTTGG TTAGTTACAA
2251 AATAAAAAAT ATGCCTTTGC CAACTCTGCG GGAAAAGCAA ACTCCCAGAG
2301 TTTGCCCTCG CTAATTTGTC CAAGTCGTGC TGTGGTTTTA GTAAATGCAG
2351 ACACGTGTC GCTCCAGCCC CATAAACCTC TCTGCTCTAG GGCTTCTCCG
2401 CCCTCCGGTG AAAGTACTG CTCGCCCTG CAGTCACCAC CTGTTCCGGC
2451 GGAACCTGCG GAGCGTGCAC CTACGCCTCG GGCTCCTTTC CTCTCCACT
2501 CCCCTTTCTT GCTGGGCACC CTGCTTTCCC TCTCCCAGAG AGGGTTTGCA
2551 ACTTTTCTCC CAGGCTGGGG CTCGCCCTGC TTGGCTAACC CCCAAGAGCC
2601 ACTGCCGTCC CGCAGCGCCC CTGCCCCCGA GTTGCTTGCC CCGCTGGGCC
2651 CCCGGGAGGA GCGGAGCGCG CTCACCCTTC GCCCGGGGCT GGGAGGGCGG
2701 CGAGTCGGGC GCACGCGCAC CCCCTGCCCG CCCCTGGCGC CCTCCCCGC
2751 GGGCGGTGCA GCTACCCCTG CAGCGCTTCC CCTAGCTAGA AGGGAGCGGG
2801 AGGGGGCTCC GGGCGCCGCG CAGCAGACCT GCTCCGGCCG CGCGCTCGC
2851 CGCTGTCTC CGGGAGCGGC AGCAGTAGCC CGGGCGGCGA GGGCTGGGGG
2901 TTCTCTGAGA CTCTCAGAGG GCGCCTCCC ATCGGCGCCC ACCACCCCAA
2951 CCTGTTCTCT GCGCGCAAGA GCGCTGCGCC CCAGGACCCG CTGCCCCACA

FIGURE 3A



REPLACEMENT SHEET

3001	TGGATTTTCT	CCTGGCGCTG	GTGCTGGTAT	CCTCGCTCTA	CCTGCAGGCG
3051	GCCGCCGAGT	TCGACGGGAG	GTGAGCTGGG	CCCCGGGGCG	CCCTCTCCTC
3101	CTTCCCGCGC	TAATTTTACA	CTCACTGTCT	TGGGTCACCT	TTCCCGCGCG
3151	GGTTTCGTGG	TCAGAGAGGC	GTCTCTCTCA	TCCAGAAGTT	GGGCCACCGC
3201	ACAGCGTGGC	GCGAGGAGAG	CGGTCCAGCG	GCTCCGAGTG	CCCGCCCGAG
3251	GCGGAGAGGG	CGCGCCCTTG	CGAGTCTGGG	ACCCCATCCG	CGGCCCCCGG
3301	AGGGCGACTC	GCCCCGGCTC	GGGAATTAGG	ACTGAGGGAG	AGGAGCCGCT
3351	GGAGCTGGG	ATCTCGGCTC	TGAGGGCGCG	GTTTAGCCAC	CTACGCCGAG
3401	GTGACGCGCG	AAACATCCCT	TACCCGGGAA	ACTCCCGCGC	CTGAAC TAGA
3451	CGGCTCTTCA	CTGGGGAAGC	TTCCAGGCCC	CCGGGGGGAG	GCCCCGGCTC
3501	TGCTCAGGGC	TCTCGGGGCC	GCTCACACAG	AGAGTGGGTG	CGAGTCAGCG
3551	ACTGGGTAC	GGGGGAGATT	TGTGGGCCTC	TCCATTGGGT	TTTCTTGAGG
3601	GAAGGAGACT	CAAAATGAGG	ACCGGAGGGT	GGGCGCTCCG	TGAATGTGAG
3651	CATGAGTGTG	TGGATGTGTG	TGTGAGAGCG	CACACACTGC	GCCGCTCCTC
3701	AGACTCGGGC	GAGCCTGACG	GCGGCGTGCT	GTGACAGGTT	CCAACAACCT
3751	CGGGCCGCGT	CTCCGCTGTC	ACTCAGCCGG	TCCTCCCGCG	CTCCGGGGCC
3801	GCTCCGGTGT	GTGAGAGACA	CTGGGTCTGT	CGGGAGGGTG	TGCTCGGTCC
3851	CCCTCACCTC	TGTGCAATTA	CAGACTAGGC	TCGTCCCGGG	TGCAGATGGC
3901	TGCTGCGAAA	AGAGGTTTTA	CTCTGGCGCA	CACCGTCGCC	CGGTGCGCTT
3951	CCTTCAGCGA	CCTCTGCCCC	CACCCCTCCG	TGTAGGTCCC	TGCTAGTCC
4001	TAAAGAAAAG	TGCCGCACCT	GTTTTACCTT	TAATCTTGA	ACGAATCAAT
4051	TCCACAATTG	ATTTCGTTTT	TTGTACCCGG	AGGCGAACGG	AGGGGAACCA
4101	GTGGAGCGCC	AAGAAAAAGC	ACAGCTGCTT	GTTCACTACC	TGGTCGGAGG
4151	AAATAGAAAAG	TTCCGGGTTA	TTTTGTACTT	TGGGCTGGG	GGTAGAAAAG
4201	CAGGTAAAAG	AAAAGGGGAA	TTGAAAAAGA	TAAGGAGACT	TTAAGAAAAC
4251	GTGATAGCAG	CCAGAGTGTA	GACCTTTTTA	TTTTATTTTT	AAAAGCAATT
4301	CTGTGCTCAC	ATTTGGGTAT	GTTATGCATT	TCTTGCACAC	ATATTTGCAA
4351	CAAGAAACCC	ATCACAAGAT	ATGCATATGA	TGTGAATGCA	TATAGCTTTT
4401	TGTAAC TT TA	AAAAGATGTC	TAAAACAGCA	AATTAATAATG	TTGATACCCA
4451	GAGGAAAAAA	GTCATTTAGG	TGTGACTCTA	AACAAGGAAA	CAATTTAGCA
4501	AATAATGTGT	CAACGTGTAA	TCAGGTGGAT	AAATCTGTAT	CCTGAAATTA
4551	CTTTCTTTAG	GCATTATTTA	CATTAGAGAG	GAAAATACTA	TGAATTGTTG
4601	ATCTAAGCAC	GTTTCAAACC	ACAAGGATAC	TTGAGATATC	AGCTACACTT
4651	TAAACTCTCC	TTGGTTTTAT	TTAGACTTTT	TTCTAGTACT	TTTTTGTTTT
4701	TTTTGT TTCT	GCCACAGTTA	TGTCTCAAAA	AGAGCTCTGT	TACACTTGAT
4751	TTTTGAGAAA	CCTTCTTGCT	CCTTCCCCCA	TCCACCTTTT	ATATGAGGCA
4801	GAAATTTTTT	CTGCTTTGAC	ATGTCTTACT	TAATACTTTT	CAGTTTATGG
4851	TGAATCAGTC	AAACCTGGCT	TTCACCCAG	TAACAGGTGT	GGGTCTTTGA
4901	GGAATCTGTT	TTATTTCAAG	CTTCAGAAAC	TATCCTGTGA	GTGGCAGCCT
4951	TGAGAA TTGT	TGGTGT TAGC	TGGTGC TATT	TCTACTTAAG	AAAGCATCTT
5001	TCCCTCCCGT	TTTTTCTCCT	ACCCTTG TGT	GTTGGGGGAT	GGGTATTTTA
5051	ACTGTCTGAA	ATTTGACATT	AGATCATAGC	AGAACTATTT	CTGTGAAGGT
5101	GTTTTAACCT	TAAATTTCTG	CAGGCATAAA	AGAGTTTGTA	GAAAATTGTT
5151	GGGTGTGGTT	GACATTTTTT	CTGAAGTAAT	AATACAGAGG	AAATTACCTT
5201	TCTTCTCAAA	AGTGTCTTTA	TTTATTTTGA	ATCTTTTTTT	TTGGTAGGTG
5251	GCCCAGGCAA	ATAGTGTCAT	CGATTGGCCT	ATGTCGTTAT	GGTGGGAGGA
5301	TTGACTGCTG	CTGGGGCTGG	GCTCGCCAGT	CTTGGGGACA	GTGTCAGCGT
5351	GAGTATCAAG	CCTGGGGACT	TCAGTTCCCT	GGGAGGTGTG	GCTTTCCACC
5401	TTGTTTCATG	CTTCACCCCA	CATATCAGAG	GGTTCATTAC	TGAGCAAGGC
5451	TTGGCCTTGC	AGGTCTGACT	TGGGGATTTT	CAGGTACAGT	CCAGACTCCT
5501	TATTCTGCTT	CTTTTCAGCT	TTAGCCACCT	GTATTACGGC	CCAGCTTTGT
5551	CATTACACAGA	GAGCCACCTT	AAATGTTTCT	TTTAGCATTT	TTCCCCCAA
5601	ATCTGCATCT	CCTTCTCTGT	TTCTTACCAG	GTTTATTNNN	NNNNNNNNNN
5651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
5701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
5751	AGATGGGGAT	AAGATAATGA	GTCTAGACCG	TATTTACACT	GGGGATAAGA
5801	TAATGAGTCT	AGACCGTATT	TACACAAAAT	AACTCTGAA	CCTTAGAGTA
5851	CTTATATAAT	CCTCACCATA	GCTGTTGTGT	AAAGTGCCCC	ATTTGTAAAT
5901	CCTTTTTTGG	ACTGGGGTTG	TATTGACAGT	GTTTTAAATG	GACCACCCAG
5951	TATAATGAAA	CAAAGCAGCT	GAAACAACAT	TATTTGTAAG	TTCTATAAGT

FIGURE 3B



REPLACEMENT SHEET

6001	AACCAACCTC	ATGTAATAAG	TACCAAATCA	GAAAGCTGAT	TTTCACCTTT
6051	TCTGTGACCA	CAAAATGGATA	TTTTAATGGT	AAAAATTAGA	GCTACATCAA
6101	AAGAGTTTGA	GAAATTTAGG	AAATTTGTCC	CCAGCATTTT	ATCGCGATCT
6151	TAAAATTGTA	TCTCACTCCT	ACTGCAAAAA	AATAGTCTTC	AAATGATCAA
6201	GTACCTTTCC	AGAGCACCCCT	TAGAGTGCTT	GGGGCGGGGG	TAGGGGGCAC
6251	TTCTGGTAAG	ATGATGGGAA	CTAAGTTGGG	TTCTACATTG	GGATATATAT
6301	TTTATTGCTA	ATGAGGAGGA	GGCTTAGAGG	AAGAGAGAAG	GGCAGTTACG
6351	AAGGCTAGAG	CTGGCAATGG	AGAAGCCTGC	CTTAGAGATG	GGTTGCTAGT
6401	GTGAGGAGTC	AGGCAAATTT	AAGTTCAGGA	AAGTTAGGAG	TTCCCTCTGC
6451	TATTTTAAAT	TTTGAGGATG	CTTGCAATGT	CTTCCTTAAT	TTTGTGAAAG
6501	AGGGACAGTG	ACAGTCACAG	ATTGACTCTA	ATTGCACATA	AAGACCACAA
6551	TCTCTGTTTG	GGAATAGAAA	GGTAAAGGAA	ATGAATGTTT	GCCTACCTGG
6601	TATGGAATTT	GAGAACCAAC	AGATTCTAAT	AACCAAAATG	TGAAGAAAGG
6651	ACCTTTCTGT	TGGCCCAACA	CACCTACACA	TAACCTCCT	GAGTGAAAAA
6701	TGAGTAGTAT	TATACCTGCA	GTCTCCAGCT	GTGCAATATC	TTCTGATACT
6751	ACAGAAAGACT	AAATTCACAC	AGGCACCATT	CTTCTTTTTT	GATCATCTTC
6801	CCTTAAAAACA	ATATTGAATA	GACTAACCAG	TGAGTGATACA	GCAGCTTTGC
6851	CTACTTCTTT	TGTTTACTGG	AAACTGGAGT	TACCACCATC	TCCCTTTAAC
6901	AGAATGTAAT	TGACCCCCCG	TGCAAAGGGT	CTAGCCAAGC	AGCTCGCACA
6951	TAGCAGTTAG	GCAAACATTC	GTTTGCTTCA	CCTTTTATGT	TTATACTTCC
7001	AAAAACAAAG	TAGTTCCAAG	GTTTTCTATG	TTACAGTGAA	ATAAAATCCC
7051	TTTCAATTAA	AAAGGCACAA	ATGGTTCTTT	ACTATTAACA	TTGAAGTTGG
7101	TGAGGTTGTA	AAAATTAGCT	CAAAGGTGAA	TGTTTCCTTC	TGTGTATTTT
7151	ATTTTTCCAG	CATCTTAGAT	GGCGCAAATG	TCTCTTGTCA	GTTTCAGAGT
7201	CTGCCTGTCT	TTGTTTTGAT	ATAAGCAGGT	AGAGGAATGT	GGGGCTGAGA
7251	AGTAAGCTTG	AAGGGGCAGA	ACAAACCAAA	AAGAGGCTGA	TCAGATTGAA
7301	TGAAATATCT	CTGAAAACCT	TTGATTATTT	TAAAGAAAGT	CTTTATGAAA
7351	TTAAAAGTTT	TGCTACTACG	TTTGTTCAAG	AAAATGCCTT	GCTATTGTAT
7401	AACAATTCAA	TCTAATATGA	TTCCCTTATA	AGATTCCAAA	GAACCTCTAG
7451	CGAATTTAAT	GTGAGAAATG	TTTTTGCCCT	TTCGACCTTT	AGATAATCAT
7501	GTAGTTCTTT	CCCATAAGGA	AGGGCTATTC	TCCCTTCCTC	ATCAGAGGTG
7551	CTCTGGTTCT	CTTCTTTTCT	GAATGATTCA	CTTTGGAATT	TTCTTCAAAA
7601	ACAGCATAGC	AAAACAAAAA	GAAACTATTC	CCATTACTGC	ATAGATCTTC
7651	CCAACCTATC	CCATAGAAGG	TGTGTTTGTA	GGTAGGGAAA	GGTGGTGGTA
7701	CCCTCAATTAT	ATTATTTAAT	AGACCTTATG	CCTTAGTGCA	GTGACCTTTT
7751	GGTGAGTGTT	TATTCCGTTT	GGTTGAGCAT	TTGTGAGATG	TTTGACTTAA
7801	TATTCATGTG	AGTCAAATGT	ACGTATCTGT	ACAAAACATG	CTGCCCTTCA
7851	TTTTCACTTG	CTATCTTCCT	ATCCATGGTC	TTGTTTGGAG	AAACCGACTA
7901	ATGTTGCAGG	ATGCTAAAGC	TGGTAGACCT	CTCCTTCTGG	CTCACTATGT
7951	CTAAGCAGAG	CCAGATATAG	CTGGGAAACT	TTATATCCTT	CCCTCTAGGA
8001	CTCAGGAAGG	AAGGATCAGA	GATGCTACTC	AAATGGGCAT	AGAACCTGTC
8051	CTGCTGCCTC	CTGCCGTGAC	CACCCAACAT	TCTATCCCAA	CATTCCTGCC
8101	TGCTAGGGAA	AGCATGACCC	GTTCCAGAAA	TAGGCAGGTT	GTGTTTTCAT
8151	AGTTCTTTTG	TAGGTCATAC	CCTTGTTGN	NNNNNNNNNN	NNNNNNNNNN
8201	ATTCTTTGTT	TTGTGTCTT	GACTCTTAAA	CAGATCTCTA	GCATATGAA
8251	AATTCAACAT	TTGATTTTCT	AACTGTCATG	GGCTTACTTT	TTATTGACTA
8301	TTGATGTGGC	TGTTTATTGT	CAGGTGAAAA	TTTTTTAATA	TGTTACACAA
8351	CTGATGATTG	CATATTTGCA	GCACACAGCA	TCTTAAACCA	CTCAGAGGTT
8401	TGTCACAAAA	TGTGTGTTTC	TTGCTCTGTA	ATTTTTTTGT	CATTTTGATG
8451	GCATATTTTA	ATTATGCTTT	TATTTCTCTC	CTTCTACCAA	GTGGAGACCT
8501	CTGTAACAAA	GATTTTTTCAG	GGTTGCATAT	TTCATCTTTA	AAAGCTGTGT
8551	ACACTGTGGA	AACAATTGTT	AACCAAAAGC	ACTAGATAAT	TTAGGATAAC
8601	TGAGTTCAAG	TTCTGACTTT	TGTACCTGAA	TAGGTGTCTA	ACATTTCTCA
8651	GCTACAGTTT	TCTTATTACA	CAAGCATATT	TCCAAGGTAT	GTTGAAGCTC
8701	TAAACTGCAA	CTGAAAACTT	CCTTAATGTA	GAAAAACTAT	ATAGGATCTA
8751	AATATTGTAT	TTTTGTATGG	TTGTCCTTCT	GTTTACTCGG	AGATTTGACT
8801	GTATATGTGG	CTTATGACAA	TAGCATTTTT	GTTAAAAGCA	TTTTATAGAA
8851	GTGTGAAGAA	AAACTAAAAA	TACAACCAGT	TCCAAGGTTT	AACAAAACCTA
8901	TTCCGTTTCT	GAGTTCCTTG	GCTGTCATTG	AGCAACTTGT	GGTTTCTGAA
8951	GGAAATTATG	TGAATTAGGA	TGGTTTTGTA	TCATTTATCC	TTAAGAACAG

FIGURE 3C



REPLACEMENT SHEET

9001	GGAAAATTGA	GATGTTTTCT	TATGTTTCTG	CTGGAGATTT	TGGAAAGATG
9051	TGAAACCTAC	ACCTACAGAT	TGACCTTGCT	TAGTTAGCTC	TGAACCTCCT
9101	GCTGCCTCTT	CCACGTAAAG	TGAAAATTTT	GGATTCTTAT	CGGCTTCAGA
9151	TAAACTTACA	GGTTAGTGAA	ACATAGGGAC	TGAGATATAG	TAATTCATTC
9201	TGAAGCTGTT	TTGGAGTGGT	CAAATAATTT	TAGTTGGATA	ATATATATTA
9251	CTGGCTAATG	ATTGTGGATA	TTGGAAGTGA	TGAAAAAATT	ATTGAATTAT
9301	TTCTTTCTGC	ATTTCAAATG	AAAAGGCTAT	TAGTTTGAGC	AGAGAATTTT
9351	GATTTAGTAA	ACAAAAATAT	TAAATTTTCA	GTTTCATTTT	TTTCTCCTAT
9401	CTGGGTTCAG	ATACTCAGTC	TTATAAATGG	AACATGATTT	ATTTTGTGCTC
9451	CCTAAACTGG	TTATTAACTT	CCTGTCCATA	ATCACAAAAC	TATATAGATT
9501	ATATATTTCT	TTGATTATTT	GGATTTTGAA	TACTCTCTTT	AAAATAATCA
9551	AGAGAAAATT	AGAGCTGTTA	GAATGTTAGA	ATTTGTTTGG	AAGGCCACAC
9601	ATAGTGTTCC	CTCCACAGAG	AGGTTATACT	AGTAAATGCC	TTTCTATTTG
9651	AGGTCAACAA	CTATGACAAC	TTCCATTGAA	CATGAGTTAG	TATTTTAAAC
9701	GTAAAGCAAT	TTTTATACCT	GTATGCACCC	AAAAAGTAAC	AGGGGCTCTC
9751	AAAAGGGGTG	GGGATTGTAC	TGTTTACATG	TATATTGAAG	ATTGCTAGCA
9801	GAATTCGGG	GCCAGCTTGG	TGGAGCGGAG	TACACTTCAT	TGTCCTTAGT
9851	GTAGTAGCTT	CCTCCTCTAA	TTTTGAGGTG	AGAATGCAGA	ATCTGTTTTT
9901	TGTTTTGTTG	CTTTTAGGTA	GGAATAAAAG	CAAGGCAAGG	AATAATTTTG
9951	ATTACTTGCA	ACATTAAACT	TGAATCCACA	AATCCTTAGG	AAGTGAAGTT
10001	TTTGATTAAAG	ATTATTTAAG	TGCCACTTTC	CTTGAAAGGT	TGTTTAAGAA
10051	CATCATGTAC	CTTTGGGTAA	CTTCAAGTGG	TCTTGGAATG	CAGATTCCAA
10101	AGTAAGATCA	GCGTTGAAGA	ATCTTGACCT	TTTCAAACAG	GTAATTGTGT
10151	AGTATGTGTA	GTCTTCAAAG	TTAAGTTTCA	GAGAAATTGC	TTTGCTCTTT
10201	TATTCCTTTC	CCCAATCAGA	ACTGATCTTT	ATGTAATACT	ATTAAGATCT
10251	ACTAATTTCC	TGAAATCCCT	TCATAAGCTT	AATCTGGCCA	GGTCTTAACC
10301	TTTATGGATT	AGAAATTTTA	GTACTTCTTA	AGCTAGAAGG	CCAGGCCAAC
10351	TAAAGGGAAG	CACCTCTCCT	TCTGCCAGTT	CAGCAACTAG	ATCTGTCCCT
10401	AAATACCTGC	CACAGGGATA	TGCTGCTTGA	AGTTGCCAC	GCATGTACAC
10451	ACTGGGACCA	AGAAGGCACT	TCTGGTGCCA	GAAACAACAC	TGTGTTTGCT
10501	TTGTGGAAAT	TTTTGATATG	CTTTAAAAAA	TGTAGGTGTC	TTCTCCCTCA
10551	CCTCCTGTGT	GTAACCTCCA	GCATTTCTTT	TTGTTGCTTT	TTATCTACAG
10601	AATTCATGTT	CTTTGCATTT	TGAGTTAGTT	GAATCCACTG	TATGCTTTCC
10651	AGATGATAAT	TAGTGAAGCT	CAATGATTCT	ATGCAGTGTC	TTTCAGTGGG
10701	TAAGGGAAGA	TATTCATCAC	AGGGGTGGGC	CTTCATCACA	GGGGAGATGG
10751	AAGGGCAAGG	GAGAGGGATT	CTGATGGCCT	AACCCCTCATT	ATTGCCCCCC
10801	ACTGCCACAT	GCAGACACTC	TTGCCGCTTT	CCCATTGATT	TTGTGCAATA
10851	TTTTAAATTT	TTCCACCAAT	CTTTGGAAAA	TATTAATTTA	TTTTGTAGGA
10901	GAAAAATGAT	TCATTTCCCT	AAATATCCCT	CCTCAGAGCA	ACAAGCATGA
10951	TTAGTTTTTG	GTATACTTTA	AAAAATATTT	TACCTACTTA	TGGGTAAATT
11001	GCAATAGATC	TCTCCCTTAT	CACCCACTTG	TTTTGTACAA	ATGAAAGCAT
11051	ACTATATACA	CTGCTTTGTA	TGCTGCTGCT	TTTTCTTAAC	TGTACATGTT
11101	GAAAGGTTTT	ATTTATAGAC	CTTCTTACNN	NNNNNNNNNN	NNNNNNNNNN
11151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11451	TCNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11551	AAAAAACTTT	GAACATATGT	TAAAGATGTT	GTTTTGCATG	TTCTTAGTGT
11601	TTCTGCAAAA	TAAATTTTAA	TATGTGGTCA	AATGGCAGAT	ACATTTGTAA
11651	TTTTTATCAA	TTGCCCAATG	ACTTCTTACT	CAGTAGAGAA	GATAGTTTAA
11701	GGGGAAAGAC	TGAATGGCGA	TGCTGACCCA	AAGGCTCCAA	CAATCCCATC
11751	TCCAGAGTCT	GATCTTTTCT	TGATTTTAGG	ATTCTTTTGG	CCCTTTTCTT
11801	TCCCAAGAAA	TCCCTCTGAC	AACTCAGTGA	ATGTCCATCT	GCTCCCATCA
11851	TCTGTTTTCC	ATCAGACCAG	AGGCAATGGG	CTGAAGCTAG	GAGAATGGAG
11901	TGAGATGTGT	CCATTTGCCA	GGGTCTCCCA	GTGGCTTCCT	GCCTATCATT
11951	TACTTGTAAC	AAAGAGCCAC	GCATTCCTTT	AGGAATTGCT	TAATTCATTG

FIGURE 3D



REPLACEMENT SHEET

12001	ATCTTTTATT	ATCTTTGTAG	TTTAGCCATA	NNNNNNNNNN	NNNNNNNNNN
12051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12201	NNTCAACTGA	TGGAGTTGAT	ATCCAGAGAC	AAGATACAGA	GATTCTGTAT
12251	CTTGNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12401	CTTTGTGTAT	AGTATGGGCT	TTTTTTTTTT	CTAGACTTAT	AACCTATTAA
12451	GGAGGAATAT	GTAGAATTCT	GAGATCTGAA	TACCATTTTG	GGGACACCGT
12501	TTATGATAAA	AAGATTTTCA	GGAAATATTA	AGACATTTT	GTACCAAAAT
12551	ACTTTTGTGA	GTGTCCTTAA	AACCATAGGG	GCATATATTT	TCTAATAGTT
12601	ATTCTAATCC	TTATTTCCAAT	TATATACTTA	AATTGTCTCC	TTTTAGAAAA
12651	GTAAGAAATG	CATGATTAGG	TGAAAAATTA	AAAGACACAT	ACTAAGAGCA
12701	AGACAGCAGT	GAAGGTAAGT	ATTTCTAACT	TTCTGTGTTT	CCTGACACCT
12751	AGTTNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
13001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
13051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
13101	TAGATATGGA	GGACATATCT	AAAGACATTT	GATTTCTGTA	TTAGTATAGT
13151	AATTGAAGAG	GTTTCATTTT	ATTGCTACAA	ATTTTCTTAT	GTTTAATCTG
13201	TAATGTAAAG	GAGAGTAAAT	CATGGCTAAT	ATTACAGAGT	AGAAACCTTC
13251	TGTTCACTCA	TCTTCTATTT	TTGATTCCTT	AGAAGATACC	TTAAAAGATA
13301	AATTAAATTG	ATTTCTTTAT	TTCTATTTGT	TTATGCCCTA	TCTTGTGTTG
13351	GAAAGTATAT	AAAGTGGCTT	CCAGGAATTC	ACACAATTAA	AATAAGGAAA
13401	TAGGGGCTAC	ATGGAGGAAA	ATGGGGGTAA	AATAAAAAATA	TTAGGAGGAG
13451	GGTTTTTCAA	ATGCAGATAT	GTAAGCCATA	GGATCCTACA	TATGTCCTAC
13501	AATTTGGCTA	CTAGCTTCTG	GTAGCCAAAG	GTAAGAGATG	TTATTGCTGA
13551	TTTAATTTGT	GTTGTTTGTC	AGGGAAAAAG	CAAACAAGTT	ATGTGGGAGG
13601	AATTATGGTT	TTACTGCATG	TAGTTCCTGAA	CGAAGACTTT	CACGTGGCCC
13651	TTTACGGAGT	GGGAGTGAAT	GATGGGATGG	AAGGGGCCAG	AGCAACATTC
13701	CTATCATGAA	GCCAGTGGTG	GTTTTTGAAA	AGCTGTTTCA	TAGAAGATCC
13751	GTCAACATAA	GATGAGGCCC	TTACTCTAAA	AGTACAGTTC	ACGGAAAGCT
13801	GTTCTATACA	TAGTTTAAAG	AGCATTATGT	GCATAGCTTT	CTGACGTTCA
13851	GCTAGATACA	GCCCAGAATA	TCTAGCTGTG	ATGGATGAAC	TGTATAGGGT
13901	TTTGGATGGA	CAGCTCTGGA	TTAGACAAGA	TAGTTTCAGG	TTAGAAATCAC
13951	TAACAATGTT	CTGAAGTTTG	CTGTATTATT	TAACAGATTA	AAGGCCAGTT
14001	CATTTTGCTT	TTCTTTTTTA	AGTCGATATA	TTTTGAAGAT	CAGTAATCAA
14051	CTAATGGAGT	TGATATCCAG	AGACATTGTG	AATAGAGCAG	GGATAGGGCC
14101	CCGCCTAGGC	TCCAGTAAAA	GGAGGATCTG	CAAAGAAATT	AGTGGGAGAT
14151	TTTTTAATAT	CAATTTTGTA	TCCATTGGAT	AGCAATATAT	AAATTCACCA
14201	CCATTTTGCT	ATATACATAT	TCATTTCCAT	GCCAGTTATG	GCTTGGAATA
14251	AGGAGGAAAG	GCATGAACAT	TGTTCCCAGG	CATCATTTAC	CCTACTGATG
14301	CTGATACATG	GATATGGGCC	AGTGAGCCCA	GGAACAACAG	AATCCCTGAC
14351	CAGTGCATTAT	TTCCCCAAAG	TTCTTGATTG	CTATAGGTGT	TCCGGGGAGT
14401	CAAAGTAACC	TCAACTGTTT	TCTTAATTCA	CCTGGATTTA	TAAGGGTTGA
14451	TTTATATAAG	TTGCTTAGAC	CTGAACAGAC	TCAAAGCAGA	GTCTGTAGGA
14501	AATACTCTGC	ATATCAACAT	CCCGTACCCA	AACCTAAGTC	ATCTTTTCAC
14551	TGGGGTGTGC	GGAAGGGCTG	ATTCTCATGT	ACTCTTGAAG	CCCTAGGCAA
14601	TAGAACCTGA	AATCCTGATG	CACATATACC	CTAGGATAAT	TTCTCTCTCA
14651	AAAAAAGCA	AATAGTGATT	TTAAAAATTA	TGACTCAATG	CATATTCTGA
14701	GAGTGCAGCA	ATCCAGTAAG	TGTCACATCT	CCTTGGGAGG	AACAAAAGAGA
14751	AGGTCTTCAA	ACGCCTTTTC	TGCAGAGACT	AGCGTGAACC	AAGAATCTCC
14801	CTGTCTGAAT	TGTACCCGTA	TATCAACGTG	GCAGCGAGCT	GAGAAAGTTA
14851	GCATTGCCAG	GGCCGAGGTT	TTCTGTCTTC	ACGGTAACAA	ACAAATGATC
14901	AGTCCTCAAA	GATAGTAAAA	TGTAGCCAAG	ATAATTGGGC	TTGAAAAAAA
14951	TTCAAAGTGA	TGTCAATAAC	CAGCTACAAC	CACAGAAAAA	TACTAGTAGC

FIGURE 3E



REPLACEMENT SHEET

15001	ATATTGATGG	TGCATCCCTG	GGAACATGCC	AGGGCAAATT	GGGGTGCAAA
15051	ATACACCAGT	TATTTAAAAA	TTGGTATGTT	ATAAGGTAAA	GAATTCATTA
15101	AGTAATATCA	AATACAAATA	AAC'TTTTTAT	TTTGATTAC	TAAACTTCT
15151	TTTTAAGTTT	TCTGATTTTA	TTACTTAATT	ACTACTGATA	CATAATTAAA
15201	GAATTATGGC	CATAATAGAA	TTCTAATAA	AATT'TCTAAT	AAAGCCAGAA
15251	TGAAGGAGTA	TATTACAGGC	CAGACATGAT	AAAGCATTAT	GATGTGTGGT
15301	AAAATAGTGA	CATCTATTTT	TTCATTCTGT	ATTATTTTAT	AAATTTTCTG
15351	GAGAATTTC	GTTTAAACAG	CCTGCTGAAA	TACTGT'TAAA	TCAACCTGTT
15401	ATTCTTAACT	CTGATGGGAG	GAAACAGATA	TGAATAATAA	AAATGATTTT
15451	TTAGCTTTAG	AATATAGTTG	TTGCTTTGGA	GAACAAACCG	TTTTATTCCA
15501	ATTATTTTTT	ATTAGGAGAC	TTCATTTTCT	GCCATACATT	AGCTTTGGTA
15551	GATACTAGAT	GCCAGGGGAG	TGCAAA'TTG	AGAATAAGGA	TTTGGCATGG
15601	GTTATTTGCA	TGTTGAGAGT	CAAGATTTAA	CTAAATTTTA	AAACCAAACA
15651	CTTCATTTGA	TCAATATCTT	TTTAACCATT	CTGTAGATTA	ATAATATAAA
15701	TTCTCCAGAG	CTTGACATTAC	TTTGCTATAA	CATCATCAGA	TCACAAGATT
15751	AGGGTTGCCT	TTTGTAGATG	TTATTCACTT	ACTCTGAAAT	GTTAGGAAAT
15801	ATGTCATCAC	AGTTTAAATT	TGTAGTAATA	TATACAAAAG	GAAAACACAA
15851	CTAGGAATTT	TGGATTTATG	CTTACTTTGC	CAAAAACCAT	GTTGATTTTC
15901	AAAAACCTTT	AGCCNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16201	NNNNNNCTAA	CCTTATTTTC	GTAAATCAAA	GTTCTTAAAT	TCAGTTTCTA
16251	AGGAAAGCCC	CTAAGTGGTC	AAAGGTGTGT	GTTGCTGAAT	TTCAGAAACA
16301	AACTCCATGG	ATGGACTTTC	CAGACATAAA	CTTCCCACCA	AAATATTGTT
16351	CCAAAGTGTT	TAGTGCCTCC	TATTTTATTT	TAGTGT'TAAG	ATTTTGTAGG
16401	TACTTGGTAA	TTATCAGCAG	AATATTTACA	TACCAACAAA	TAGCAAAGCC
16451	ATTGATAAAT	AATAGAAAAA	CAAAATCATA	GCTTATGTTT	AGTTGTATTT
16501	TTTAGTGTAT	TTCAGTGT'TT	AGAGTTGATT	TTATATTGCA	TATACTAACT
16551	GTGGTAATAG	TTTCTACTGG	ATAGATTATT	TCAAGTTCAC	ATGATTATAG
16601	AAGTATTTTA	TGAAGTTTGA	CATAGATAAT	GGTGGTTTCA	GGGTCCCTTG
16651	TCTCTTGGGT	TGAGTTT'TTA	CATCATTGAA	GAATTAAAAG	ATTGTGTCTT
16701	GGTGTCTATG	TAGTGCCTAG	AATTAAGACA	TTCTGATGTA	CAGTTTCATT
16751	TTCTAACTAA	GGCAAAAATG	ATTTT'TGAAA	CAATTACTTT	TTAGGATAAA
16801	AGTATAAAAT	TATGAAGAAA	TAATGTGTAG	GTTTGC'TAAA	TGTTGTGTTC
16851	TTAAATCTTG	TGTTGAGGTC	TGATGAATTT	TTTTATATCT	TTAATAGTTC
16901	TAAAGTAGTG	TACTGAAAGT	TAGGATCATC	CATGTTGCTA	CTTAAC'TTGT
16951	TGTCCATAGG	GTCTGTTGTC	CTGGATGTTG	GTGTTATAAA	TGTACAGAGT
17001	TAGGTAGTTT	TCTGTGAAGA	GTTTGCAGGC	TAATATCACT	GTTTTTGACA
17051	ATGAAAAATA	TAGCATGAAA	ATTAAGGTTG	GGGTATGGAG	AAC'TTCTAG
17101	AGCTATTGCT	TTTTCTAGCT	GATGATTAAG	GTTGAGAGGC	AGAAGTACAT
17151	TGTGTCAGGG	AGGACCTTTC	CCTTTTATGC	ATGCACCTGG	CATTTATCAC
17201	CTTTAACAAA	GTGTGTGTGT	CATGCTGTGC	TGCTTGCTTA	AGGGGCTGTA
17251	TGCCTCCAGT	CTGAGTCACA	TGGTAACTGC	ATCAGCAGTC	TTAGCCTGTA
17301	GCATTTTATT	ATTTCTTTTC	AAAGTTTACA	CTTGGCCTAA	TACTTAGACA
17351	TTTTATAAAT	CTTTACAGTA	AATGAAACTA	TACATGAGAA	GATGGGCATA
17401	CCTTTGGATT	AAAAA'AAAAA	AAGGCTCAGT	TCTTTAAAGT	TTCTTATCCT
17451	TGATTTTCCT	AACACGGTCC	AAAGTTCAGG	ACTGGCTCCA	AACCCATAAA
17501	CCTGTGTTTA	GCAAGCAAGA	AACATAATCC	CCAGATAGTT	TAGTTTCTCT
17551	GGTTTATGAG	TCACAA'TTTC	ATAAAATCAT	CAGAGTGCTT	ATTAAT'TCCA
17601	ACCACGTATA	GTAAAGAACC	TTCAGATGAA	CTGAAGCAAG	GGTTC'TTAGG
17651	CAAGTTGCCG	GAGAGAGTTC	TAGAATTCTA	AACTACCTGA	GTAGCTTTGC
17701	TGAAATGTTG	CTTGATTTTG	CTACTGTGGC	CATTTTATGA	TGGCCATAGA
17751	GCAACAGATT	ATCAAGAGAA	AATGAGACAG	ATTTTCTGT	ATTATGTGCT
17801	ATGAATGAAT	CCTATTTTAG	TGAATGTTTT	AATGGGGTTT	ATACCGCAAA
17851	AAAAA'AAAAAT	TGTATGTAAG	GCATTTATTT	CTGGCAACTT	TCATAAAAAT
17901	TGTTGTGATG	GTTGCATATA	AAAATTTCCCT	TATCCTTCAA	TAGAGGATAG
17951	TTCCAGAAAA	CTTCATAGAA	GTAATCTATT	CCAGATTTAA	CATTGC'TTGT

FIGURE 3F



REPLACEMENT SHEET

18001	ACATAAAATG	CAGTTTGTG	TAGTTTAAA	ATGCAAATTA	AAAAATATAG
18051	GACATTGGCT	AAAATTTTAT	CTTGAAGTCG	GGTATATATT	GATACCATAA
18101	AACTTACTAG	ATCTATGTAT	TTCAAGGCTA	ATTTATGCCA	AGTAGGAAAA
18151	ATATGACCCA	ACCTTAAGAT	ATTACAAGGA	TAAAATAGAC	TATACAAAAC
18201	TGTTTGGCTA	TTTGGTACTA	ATACAACCTAG	TTAGAACATA	ATGATGTTTG
18251	CTATTCTTTA	TTAAGTTGTT	TTACCTTTGC	TTACAATAAT	TTAAAGTATT
18301	TTTCCTGATA	AATTTGATGA	CTCAAAATTG	GCAATTAAAG	AATATTAAG
18351	AAACGGTATC	CTTTTATATT	TTTTCTGTCT	CATATATAAC	CATAGTCATA
18401	ACTTGTGTGA	TCCAGAATGT	AATTTGCTAT	TTACACTTTG	ATTTCACTG
18451	TTTGCTTAGA	TTGTACCTGA	TGTATTTTAT	TATTCTATTT	AAGGAATGTG
18501	TCAACATCAA	GATATGGTGA	GTTCTTTTCA	AAATAACAGT	AGAAACCTGA
18551	CCAATATGAA	AAAAAAAAGT	CTAGCAAGCA	AATGTAATTT	GTGCTTTTAA
18601	AAATACATAG	CAATCATTCT	GGATCAATAG	TTAAATTATT	GCTTCAATTA
18651	AATCAAATTG	GACTTAGAAT	TTTTTCTTTC	TTATATTACC	CAAAGGAAGG
18701	CCCCATTCAC	CNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNA
18751	TTGTAAATTA	CAGTGGATAT	TTAATCCTTT	AAAGGCATTA	ATTTAGCAGA
18801	GAAGAATAAA	ATTATCCCTT	TTCTTACCTC	TAAAATCTCT	AGGTTGATCA
18851	AACACTGACC	ATTATTAGTA	CCATTTCAG	TTTCTCCCT	TTACTTTCAT
18901	CAAACCTGGT	TATTTATGTA	TGTTCAAGTG	AAATGGCTGT	GCTTTCATGG
18951	TAATCTTGT	TGCTATTGAC	AACCAAAGCA	GCCATGCAAG	AAGAAAATGC
19001	TGTGGAAGGG	AAGAAAAAAA	TTATATTTCC	TCCCCAAAGT	TGGAGAGAGA
19051	AGGGAACATA	CAGTATGTAA	GAAACAGGTA	AGTAAAAATA	TATCAATTTT
19101	AAAACATATTA	GCCTTCTT	CTAATTGATC	AAAAGTTTAA	ATTTTTCAG
19151	ATGTGTTTTT	CAACTCCAAT	TTAAATAAAA	GGATACTGTC	TCTAGGAATC
19201	AGAAATTAAT	ATTCTGGAAA	TGAAAAATTG	GATTTGAAAA	TACAGCATCA
19251	CAAAGGTCT	GAAATATTTA	AATTTAGAAT	TTGGACTATA	GAAGAATAGC
19301	ATAACTTCAA	TTATTGGTTA	ATATTTTGT	TATGAAATGT	TTTTTTATAA
19351	CAAAATGGTG	ACTAAATAT	TACTATTTTA	AACATGTCCT	AGATTTT
19401	TTGTTTCAGA	AAGCACTGA	AAGTTGAATA	TGTGTAAGTC	TCCGGGAATG
19451	TAACAAGTTG	ATAAATACCC	AAGTCCAGCC	TCCTTACAGA	GAAAAGATCT
19501	GGAAATTTCT	TTTTTGGACA	TTTGTTTTGC	AGCTTCTAC	GTCTTAAGGC
19551	AGAGAAATAGC	CAGGATAAGG	TGCCAGCTCA	AAGGTAGAT	GAACATATTT
19601	CTTGAAATAA	TTTTGGCTAA	TCTATGTCTT	GAAAGGCATA	CCTCTAAAT
19651	AATTTTACAA	AGCTGTAAAC	AAAACATTAG	TTGTGTTTTT	GAATTGCTTC
19701	TTTTTAGGAA	AACTATATTT	CTTAGAGATG	TGCTTATTCT	ATACATAATT
19751	ATAGTAAGTT	AATTTTAATT	CCATTATTAC	ATTAACCTTT	TCCGTTTCAG
19801	TTGATTATTC	CTTCTCTCTG	TTTTATGAAT	CTAATAAATT	GACCTCCATT
19851	CTAAGCTAAA	GGACAGTTTA	TGTTTTTAAT	ACTTAAGGAA	GCAAAATATA
19901	AAACAAAGTC	CACCAAATGA	AATTACTAAC	ACCAGCCTAT	CATTAACTTG
19951	AGGGAGTTGT	ATTTTCATATT	CATTAAATCT	CCATGGAACA	ATTCAGGTAA
20001	GAAATATTTT	TATTTGTATGA	AATATGTTAT	CAGTTATAAT	AGCACTTACG
20051	GGCATTTATG	CTCTTGTTTT	AGGTACATAA	AGGGTTCCTT	GTTTAAGATA
20101	TTTTTGGCAG	TAAATAATGT	CACCTATCAC	CCTATGACAC	TTTAGTGGA
20151	AACGTTGGTG	AAATATGTGG	AATTGTAATG	TTTAATGGAA	TTGATTCTAA
20201	GAAGACAATG	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20501	NNNNNNNNNN	NNGAGAAATG	TCTTTAAACT	GATTGAAGAA	ACTATCACAT
20551	GTCATGAAAA	ATGTTTTTAA	GGCAGNNNNN	NNNNNNNNNN	NNNNNNNNNGG
20601	AACAAAATTG	ATAGTACTAG	AAATAGAAGT	TCAGAAATTT	CTTTGTTTCTAG
20651	GGAGACTTAA	AGCATATGTA	TTTTAAAGTT	ACTAGCAGTT	ATAGGATTGA
20701	CTAGTAGAGC	TATGGCTTAC	ATTAGGGAGG	CAATGCCAAG	GAAAGAATAG
20751	AATGTGTGGT	TGGCCACCAA	CATNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20851	NNNNNNNNNN	NNCTAACTTT	GCAAGATCTT	TACTGGTTAT	AAGGAGGTGG
20901	CTTCCACAGT	TCTTGACAGA	TGTTTGCTAT	TATTAGTGTG	TTCTCAATAT
20951	ATACAATACA	AATGGAGAAC	TCTGAGCCGA	GTTTACTAG	GATCCATCCT

FIGURE 3G



REPLACEMENT SHEET

21001	AGGACAGATG	GTACAGCACA	TTTTCAAATG	GTTTTGTTTA	CCATAATCAT
21051	CTTTTGGAAA	TAATCAATTG	GAAGTAGAAC	AATTCTTCAG	TTATTCATTT
21101	CTAAAATCAA	AACTTTCATG	GGATAGTTTT	CTGTGCTTCT	GAACCGTTTT
21151	TCCCATTCT	CTAATAATAT	CCATCCATAA	ACCTCCGAGT	GGAACAGTTT
21201	TGGTTGTCTA	ACAGTGTG	TGCTTGGGAA	ATGAATTGAA	GGGAGATGGA
21251	ATTGAATTGT	TGAATGTGAG	CATTTAGAGT	TCCTGTAATT	TATCCGTNNN
21301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
21351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNTTG
21401	TAAGATGATT	GGCTCTTATT	CCTTCTATGA	TTCTTAAATA	GGAAAAAGTT
21451	AGGGATAAAG	ATTTGAGGGA	GTTCAGGGAA	AGAATCATT	CCTGCTGAAG
21501	AGGATCAAGG	AAGACTTCAT	GAATCAATG	GTATTCAGTT	GATACTATAT
21551	ATATATATAT	TATCAGTATA	TCTAGTATAT	AGTATCAGTA	TTGAAAGCCC
21601	ACAGAGGAAG	GCAATACTGG	GTAAGAGGCA	TGTTTATAGTA	TAGGATTCTG
21651	TGAGAGCATA	TCTTAAGGGG	CAGTAGCCCA	GACCAGCAGT	GATGGAGTGG
21701	TGATGGCCCA	GCTGAATCCC	GAGGGATAAA	TCAGTCAAGT	GAAGAGTATC
21751	CTGGGCACAC	AGAAAAATGC	ATTTAAAGCT	CAGTAGCCAG	AGGGAGGAGC
21801	ACATTCGAG	AACTGTTAAG	AATCTCAACC	CAGCATATGT	GGGGTATATG
21851	TTTGAAGGGC	ATCTGATGAG	AGACGCAGTG	GGAGAAAGTG	GAAAGGACTC
21901	CTGGAAGGCT	TTTGATATCA	TATTAATAAC	ATTTGCCTTA	ATCACAAGT
21951	TGTAGAGGAA	CACTGTAAAG	ATTTTAAGCA	GAGAAATTA	TATTTTAGAG
22001	GATAGCTGGT	GGTAATGGAT	CAGATCTAGC	ACTCAGGTGA	ATTTAGTTTT
22051	GCTTGGAGTG	TTTGTAGTTG	TCAGTGTCTC	ACAGGAGACA	CGGATATAAG
22101	GGTTGGTTCA	AAAATCGGTA	GGTCTGCATT	GCTGCGAGGA	GTCTATCAGC
22151	TGGGGCCTCT	TAAGTAGCTG	GCCCATTGG	AAGAAGTATG	TGCCCTCATTT
22201	CCCTGTGGAG	CTCACTTCCT	TTAGTGCAAA	TGCCCTGGAC	CTGTAGGAAG
22251	TCAACCTGGT	GAGAAATTAG	GCCTCATTTT	AAGTAGTGGT	GGTGGGAACA
22301	AAGAGAAGGA	GAGGGATTGA	AAGATACTGA	AAAGAAAGGA	TGGAGAGGCA
22351	CACAGTGTTA	GGGCAGTGGC	GGGGGGGCAC	ATGGGCTTGG	CAGACAGACT
22401	TGNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
22451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
22501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
22551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNCAGTATT	TGTAATGCTG
22601	GTTGTGAAAG	GTGAAGAAGA	TGTAATCAAG	ATTACTCCCA	AGTCTCTAGG
22651	ACATCATTTG	GTGAGCTAGA	GAACACAGGA	GAAGGTGCAG	ATAATGATTT
22701	CAATTTTGA	TATGTTTCAGT	TTGAAGCGCT	TGTGAGACTT	TGAAGTAGAG
22751	AAACTTGATA	TGTGCTTGGA	TTGCAGGGTG	AGATCTGAAC	AGAACACAGG
22801	CTATGATTTT	ATTTCTTTCC	ACTATTCTAC	TCAAACCTTC	CTTCCTTTTC
22851	CTTCGTCAAC	TTCACTCAAC	ATTGATTATT	GCCACAACCTA	TCTCCACGGA
22901	GGAACAGCTT	TAAACAGTAG	AAAAAGAATG	TGGGATAGGT	AAAAATCTGT
22951	GTTCCACATC	TGCTAAATGT	TATCTAATAG	TTGTAAGTTC	TTGAAAAAAA
23001	ATCTTTCCAG	TTTACCGTTT	TGGCAAAGCA	TTGTAAGCAA	CTAATAATTC
23051	AACATTTGTT	TATATCAAGG	GCTGAAAAAA	AGTCATCCTC	TACAAACATA
23101	TTTTCTTTTT	TTCCCTCTTT	TGGTTGCCTT	TTTTTGTTTT	ACATCACCAC
23151	CACTCCTAAC	TCTAAGAAAA	TATTTGACTA	AAAGTGAATC	ATTGTTAGTA
23201	GTGAATTCGT	ACNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23501	NNNNNNNNNN	NNNAGCACAT	TTATTTTSTA	AGTTTATATT	CTGTCTAAT
23551	ACAATGTATT	AAAAATGAGC	CCTGCCTCAA	GTCCTAGCCT	AAATGCCACT
23601	TTCTCCAGTC	TGCTTTCCTG	ATTTTCACAG	CAGGAAGTCT	TCTGTACTTC
23651	CTCTACATAT	AACACTTGCA	TGAAGCATAT	CTCACATTGC	CCTACATTGT
23701	GGTTATTAT	GGATCTATAT	TATTTGTCT	GCTAGACTAT	TAGTTTCATG
23751	AAGGTGGAGG	CAGTGTCTTA	TACATCTTTA	CGCCAGTATA	ACAGCTTCTG
23801	CAATGCCCTCG	TCCAGTTCAG	TTCACTACAC	TTTTGAAGGT	GTAAGAGCTA
23851	GTCATTTCTA	TTTATTAATA	AAAGGGATTT	AAAAAAAGA	TGGACAAGAT
23901	GTAATCTTAA	TAAACATATT	GTGGTTTCA	GGAAACAGTT	TAATGAGAAA
23951	ATGAATATAT	TTGATCCCT	ACCTTATGAC	CTTATTACAT	ATCATAGATC

FIGURE 3H



REPLACEMENT SHEET

24001	TTCACCTCTTG	CTTTAGATTC	TAAACAGAAA	TCAATTTATG	TGCTTGAAAT
24051	CACATAAAGG	TAATCTGATT	GTGTCATCTA	CTGCTTACAG	TCCATTGGCT
24101	GTTCACAATT	ATGGGTAGAA	TCTTGATTAT	TTGAGTAGAA	GCCTTTTCAG
24151	GCTGACATTG	CCTTATCAGT	GGAGGACTGT	TTCTTGTGTG	AGGCCCAGTC
24201	GCAGTGGACG	GCCCTTGGGT	TTCCAGACTT	CTGCTGCTTC	ATGCCTGTTG
24251	GCTTTTCTTA	TGCTGCTCAG	TCTGAGTCAA	AGGCCCTTCA	CCCATTTCCCA
24301	TGGTGAATTT	CTACTTATCC	TTTAAAATTC	AGCTCACATT	TCCTCTTGAA
24351	AGTTTTTCCT	GGTATCTTTC	CTATTCCTGC	CTCCCTGCAG	AGAAATGCCT
24401	TCTTCTGTAT	TCTTTTAACA	CCTTGTTACAC	CTGTCATGTC	TATCTTTGTC
24451	AGGAGACTGT	ACACTACAGA	GCAAGTACTG	TGTATTTAAA	GAGCTCAAAG
24501	TCTAGTGAAG	GAGCTAGATA	AGAAAAACAA	CTCTGAAAAT	ATGGTATAAG
24551	ATATATATAT	TTAAAAGTAA	ACCTGTATAT	ACATATAATT	TATGATAGAA
24601	GTATGCACAG	AGGCTTATGA	AAGCACTGAA	GAGGGTATGA	ACTCAGCATG
24651	AGGCGTGAAA	ATCTTGGGGG	TGATATAATG	GTCAAACCTGA	CAGGTGAAGC
24701	CTGTCTAGAT	ATTAGTGTAG	CAGACAAGAG	GGGGAATGGC	ATTCCATGTG
24751	AAAGTGTGGA	GGTACTCGAG	AGTGTATTTT	TAAGAACTGC	AATTAACATG
24801	TATATTTGTG	AATGTGATTG	GAAATGAGGC	CAATGGGATA	GGCAAGGGTC
24851	ATATCATGAA	ATATGGTACT	GAATGCCATG	CTGAGTGTTC	GAAATAGTAT
24901	AATGATCTAC	ATGAACATGA	TGAGGAGCCA	GTGAATGAGT	ATAAGGAGCA
24951	GAATGGCATG	CTGAAATCAT	GGGTTAGGGA	GGTCCCTCTA	ACAATAGTTC
25001	AGGCCTGGAT	TGAAGTCCAT	GATGTTGGAC	ACAGAAAGAC	TGTNNNNNNNN
25051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
25101	NNNNNNNNNA	AGGTCTCTCA	ACAGATAAAT	TTGGAATAAT	TATCATTTTC
25151	TTTAGAAAAC	AAATAAGCAA	ACTAAAAACA	CCTGAAGGTC	AAAATGACAA
25201	ATCTCTGACA	TCATATTAGT	CGAGGCCCAG	TAACAAAATT	GNNNNNNNNNN
25251	NNNNNNNNNN	NNNNNTATAC	TTCAACTCAT	GTATCAGTGA	CTCTTTTAAA
25301	CATAGAGATT	TTGGTTGCTA	AAAAAGGTGA	TGATGGTTAC	ATTAAAAATTT
25351	TCTGGCCTTT	TGTGATGATT	CTTTAGCAAA	CCTGCTCAAA	ATTACAGTAT
25401	CAGATGTTTT	AAAAAATGAT	AATTTTCAAC	TGAAAGAAAT	ACTGTAATGT
25451	ATTTTCATCAT	ATTCTATGAA	TTCTTACATT	ATGAAAGATA	TCTTTTATGT
25501	TTCAGATATC	TATTATATTT	CCTTTTGTAA	AGAATTTTTT	CTAGCACTAC
25551	ATCTTTTCCA	AACCTTTTGT	ACTTTCCTAA	GCCTGTGTAA	TTAATCACTG
25601	CCTGTTCTGT	GTCTTAAACA	TGCATCTGTT	ATCAGGACAT	CTCTGCTTAC
25651	TTCTGTTTCT	CCTTACTAGA	CTTACCTGCT	GGAGGATGAG	AACCTGCTCT
25701	CCTATTCTAT	TTTATATCCC	CAATTTTAA	TATAGTGTCT	TAGACACTGG
25751	GGCGTTTCTT	CCTGTGCATA	CTTATAATCC	TCNNNNNNNN	NNNNNNNNNN
25801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
25851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
25901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
25951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNCCCT	TCTCTAAATT
26051	ACATTGAAAA	GTTAACAAC	ACTCACAAGT	TAAATAATAG	TTGTCTGTGT
26101	ATTCATGTTA	TTGTACTCCT	TTTTATATAT	TTCTTCCATG	NNNNNNNNNN
26151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

FIGURE 31



REPLACEMENT SHEET

27001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNTAC	TCTACTNNNN	NNNNNNNNNN
27401	NNNNNNNNNN	TTCACATTTT	CAAATAAATA	GTAACACTTT	TTAATGTGTT
27451	CTTAACGTTT	TATTTGGCAT	TAATCTAAAT	TCCCCCTCTAG	CACAATGAAA
27501	ACAGAAAGAG	AAAGTTAAAA	TTTCAAGTAA	ACTGAAAACA	ACAATAGTGC
27551	TCAGAGGATT	TTTTTTTAAAG	TGAAAAGGGA	TAGTGCTTAA	TTATGACAAA
27601	TAAAAGCTAA	CTTGAGATGC	ACATATACAG	ATGCAGCCAC	TTATTTTGGC
27651	GGGGGACACT	TCAGGAATTA	AAATTTAAAT	AGCGAGAGAT	CAAAATAGATA
27701	CTTGGTAAAT	GTGTCGAAT	TGGATGTTCC	CAGACACAAA	AATAAAATGA
27751	GTTATTGACA	GCTCTTGGGA	GACAACATTA	TAAAGACTAG	ACACGTTATT
27801	TATTTTAACT	CTATGTTCTA	AATTACCATT	GAGTAATTGA	CATTCGTATT
27851	TGACTATGGT	TTGTGGTTAA	GTTCTTAATT	GCAATAATGT	TAAATAAAAT
27901	GTGAAGCCCA	AAGCAAACAA	CAACAAAAAT	TATAGCAATA	CTTCAACAGA
27951	GGTAATAATA	ATATGCTGCA	TCAATGGTTC	AGAATCCAGC	ATCTACATAA
28001	AACAAGCAAC	AGGGTAATGA	AATTATTTTC	TTTTCAAATA	TTCTGGCAGA
28051	GCTACTTTTAG	TTTTCTTAAG	TTATAGATTG	TGGTCTTAAC	TGCAACTTTT
28101	CGCTCCTTTT	AAGAAGTATT	TAAGTTATTT	AAATGTTACT	TAAATACTTT
28151	TATGTTTTTA	ATCATTATTA	ACATTCTCTA	CCCCCTCAT	CCTTTCCTGC
28201	TTAGTATTTT	GTTATAATCT	CACCTCTCCC	ACTTCCAAAT	GCACTCAAAA
28251	ATGCTGGACT	TTCTGGTCTT	TTTCTGACCA	CCAGAAGAAG	TAGTGGATTG
28301	AGCATGGAAC	TGGGATAAGA	CATTTTTCN	NNNNNNNNNN	NNNNNNNNNN
28351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
28401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
28451	NNNNNNNNNN	TGAGTTCTGT	ATTCATGAGG	GCATTTAATG	TGTCTTATAG
28501	TGATAACAAT	CAGAGGCATT	ATTATTCAGT	TTTTACTGCA	GCAGGAGTTT
28551	AGATTTGACC	ATCAGATAAT	TGACACTATA	GTACAGGGTA	TTAGGAAAGC
28601	TGGAAAGATG	CTTTCCTCTG	GAGATCTTGG	ACAGTAGGAT	TCTTCTAGGT
28651	TTTGTCTGTC	TCATGATATG	CAATGGCTCA	GGGCACTTTT	CAGAGGACCA
28701	CTGTACAATC	TCCCTCCATT	CCACCCAGGT	CCTATTAATA	TAGTAGTGAG
28751	TTGTTTTATA	TTGCCCTCAG	TGACTTTCCC	TTTTTCCAAG	CCAATTACCA
28801	TTTGAAAAAG	TCATTCCTCG	TCATATTTTC	TTGTTCTGCT	CAAATGAATT
28851	TGTCCATATC	TGAATCTGCT	GAAGCTTGTT	GGGTGTAAAA	ACAGCTTTTC
28901	AAAGTCTTCC	AGTTTCATAT	CTATTTGTTC	TTCTGCCCTA	CCCTTGCAATG
28951	TTTCTCTGTC	CCCTTTTCTT	CTGTGAGCAT	AACCTGGAGG	ACAAGGTTTT
29001	TTGTTCTGCT	TTTAGTGGTG	CCATGTCTGT	ATAATAACAT	GATGTAGATT
29051	GAAAAAATTA	CAAATGATTC	TTGGAATTCT	AAAGATAATC	TTATTTCTAT
29101	TGAGAAAAATC	CTTCTCAAGT	TACTAACTAC	CATTGAGATT	GGATTGGCTT
29151	TTGCCTTATT	ACTTTTCAGA	GCCTCCATCT	GCTTGGGTAT	CTCAACATAT
29201	CCTTAGTTTT	CAAATGTGG	CACCTTACTC	CCAGCATGAT	TACCTTACAT
29251	AAGAAACATT	ATAGGACTGA	TGTGGGAGTT	TACTTTTCTC	ATAACTTATT
29301	TGATAAATCA	CTGCTTATGT	TAGAGTTAGA	AACTATTGTC	CAACTCTCAG
29351	AGACCCAGTT	ACATCACTTA	AGATGGATAN	NNNNNNNNNN	NNNNNNNNNN
29401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
29451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
29501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
29551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNGGAT
29601	GGATTTTAA	GACTAAAAAT	TTAGATTGCA	ATCAAACAGA	AGAGGCTTGG
29651	ACATGTGACA	TTAAAGAGCT	ATGTTTGTTT	TGCCAGTTGA	AACTTGTTTC
29701	TTTTTCTAGT	TAAAACAATG	ATTTAGAGGT	TATTTTGAGG	GCACTTTGAA
29751	GATTATGCTA	CAGGAATGCT	AGAGAGCAAA	TTTTTGAGAGT	GATTGCCCCAT
29801	TTGGACTTAA	TTCTGGCAAC	TGATTTTGGG	GTAAAAATGTC	TATCATTCGT
29851	TGATTATCTG	TGATTTTAC	CTGGACTTTA	CTTAAGCTTT	ATTAAGTTGC
29901	TAAACCATAT	TTGGATGCTA	GTGATAGCAG	ACCATCAAAT	ACGGCCCAAA
29951	CTTCTTGTTT	TGATCCATTC	GAAGGTCAGA	GAAGCAATGC	TGCCTTTTCT

FIGURE 3J



REPLACEMENT SHEET

30001	GATAGCCAGT	AGCACCAGCA	GGCACGTTGT	T TACTCCAAA	CAAGAATTTT
30051	AATATTTTTG	AAGACCACTG	AAAATGGATC	ATTTTACTTT	TTTTATTTTT
30101	TTGATAAGGA	AGGGATGACC	TACTATTAC	AGAGTAATGC	AGTTTGCTGA
30151	AAAGGTTGGT	TTTTGCTGAC	CTCTGAGAGC	TCACATTACA	GTGGAGTGTG
30201	TTATTGGAAG	GTGAGCCAGT	TTATACAGAG	GTTGGGAATT	ATTTTCTCT
30251	AGTTTTGAAA	TGGTTATGCA	CTTCTAATC	TAGTTATTTA	GATGTAGAAA
30301	TAAAGTTTTT	TTTTTACATT	CCCCTGAGTA	TATGGTATTG	TAGGTATAAA
30351	ATAAATTTGA	TGAGTTTTAT	TTCTGTACTA	GGATCTACTC	ATAACTCTTC
30401	TATCCTAAAT	TTGTATCAAA	AGGAAACCTT	TGCTGTCTTG	ATAATAAACA
30451	CAGACTAAGT	CCAGATTCCA	CAGTCTAGTG	ATCAAGGAAA	TTCAGGAATT
30501	GTATTTAGCT	ACAAGTAACG	TGACACAAAG	AACAGTGCCC	TAAATTGCTA
30551	GGATGGTGAT	TTAGGGTTAA	TATTATGACT	TCTTGCTCTA	CCCTCTTTCC
30601	ATTCTCAAGA	TCGCCTCATG	GTCATAAAGA	GGCCACTGTG	GTTGAGTCAT
30651	GACATGCACG	TTCTAGGCGA	GAACACAGAA	CAAGCCGTGC	TCTTCAGCCC
30701	CCTTCTTACA	CAGCATTCCA	AAGCCCCACC	CCATCACTTC	TGCTTTCATC
30751	CATTTTAGCC	AGAAGTTAGT	CATTTGGCTG	CCCATATCTG	CTAAGGAGAA
30801	TAGGGAACAT	AGTTTTCCAT	TACTAACCCA	TCCCCCACTC	NNNNNNNNNN
30851	NNNNNNNNNN	NNCCATTCTA	TATTAAAGCA	GAAGGGAAAG	AGATATTGGT
30901	AAGAATCCAG	CTGGCCTTTT	GTGATCTGTG	TCAGCCTTTC	TTTTGATCTC
30951	ATCTGCTGTT	TTAAGCACTT	TACACTGTAG	CCCCACGAGA	ACACTTTGCA
31001	CTCACTAAGA	AGCAGTCCCC	TTTGCTGCGC	CCCCCCCCCA	CCACTTTGCT
31051	TATATTCTGA	AGTCTTTTGT	TTTCCTATTCT	CACGTCTCTT	ACCTCTAACA
31101	CACTGCCCTCT	AACACACCAA	CCTGCAAGTTG	TAGTTATTAC	ACACCCTCCT
31151	TGGTCTCTTC	ATCTCTCTAT	CACAGCCCTT	GTTGTGGTTT	AGCCAATATA
31201	TTTTAGTTCC	ACAGCTAAAT	TTTCATACCC	TCTATGACTC	TCTAATCCCC
31251	TGCCACACTT	GCCTACTATA	ATACATTATA	TATATAACAA	ATGTTTGATA
31301	CGTATTTTAT	GAATCCATT	CCAGAACTAA	TGCCAGCAAG	ATAACTTTGT
31351	GCTATATAGG	AGAATATCTT	TTTGTGCAAC	AGTTTCCAAA	GGGTTTCTT
31401	TTTTCTAAGAA	GAAAGAAATT	GATTGTATCA	ACTTTATGAG	TATCCTACCG
31451	CATTTAATAG	CCATTGGCTA	ATCTAAGGGT	TCCTGGTTAC	TTCACTGAAT
31501	AGCCTATCAG	ATGGAAGTGC	AAACAACAGT	TTGTTTGTGA	ATAGGACTCC
31551	CTAAACATGG	AAGAAACATT	AACAGTGTG	GCCTGTTGGA	ATGTGTGCAT
31601	TTGATGTGCT	CAAGATTAGG	GCACCTGCT	TGAGAACAAA	TAACAAAAAA
31651	GGGAGAGGAA	ACAATAAAAA	CTTTGGTCCT	ATAAAGCACC	TGAAAGTACT
31701	ATAAATTGAT	GGTCTCAAG	CTGGTCAGGG	GGTCCAAAGG	CTACAGCCTG
31751	GGGGCCTCAA	GTTTAATTGT	TTTATAAAGT	GTCCCTAAATA	AAATTTTAT
31801	GTTTTTAAAGT	GGTATTTTTA	AAACTACTTT	TTCATGCTTT	GAGAGAGTTT
31851	TCCAAATTCC	AATTATTTTA	AGGGGTATT	TCCTGGACTT	GCACTTAACG
31901	ATTTTGAGAT	GTTTACATTT	TTTTCAATAT	GGCATTCTGT	GTGCCTCAGT
31951	GATACATGGT	TATCCAGGTT	GCATGCATAT	ATAAATGTTA	AGATTTATGG
32001	AAGGTCATCT	TTTTAGATTA	AAAAGAATTT	TTTTAAGCTG	GTATTTCTTG
32051	GTGATAGGGC	TGTAAGATTA	TGTAGAGTGG	CTTACTTCTG	GAACCTATTT
32101	TAAACTGCAT	ATAAACCATC	CGCCTAGTGT	ACAGTTGGCT	AAAGAGTAAT
32151	ATTAGAAGGC	CCTCCTGGAC	AGTTTATTTT	ATTTTCATGGA	TATGAACACA
32201	ATTGTTTCCC	TTTGAATTTA	ATGCCATGTT	TAAATCAGA	TTTTAAGAAT
32251	TTTCCAAGGG	CATTTCCCTA	TCATTTACAC	TCTGCTGTG	TTTTCTTTCT
32301	GTAGTCTTTT	ACATTAATA	CCTCCTACAG	AGCACTGCCT	AAGGATTTGT
32351	GGTGGTACAG	GGTCCAGTTG	GGATGACAAA	CAGGCAAGGA	AGGCCTGGAA
32401	GTAAAAATTAG	CAAAGAGGCC	CTGTGGAATG	GAAGGTGAGG	GAAGGGTTAG
32451	TGACAGTTGG	GGGAGGAAAG	GTAGAAAAAA	AAATAACATG	CACATCAGTT
32501	TCGCAGGAGT	ATTAGAGTCT	TAAAGGAAAC	AATGTTTGAT	AATTATCAGA
32551	GAGGAAACTG	GGAGCATAGA	GCATATCCCA	GAATGGAGAA	CAGCATGGGT
32601	TAAATGGGT	AGGAACAGGT	GTCAGGAGCT	TCAAANNNNN	NNNNNNNNNN
32651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32951	NNNNNNNNNN	NTGATTTTTA	TCAGGCAGTT	ATGATGATAA	ATGTATGGAA

FIGURE 3K



REPLACEMENT SHEET

33001	ACTTCCCATT	TCCTAGAGCT	AAAGTGCATG	TTTCTCATTC	TGAAATGTAG
33051	GGAACATAAT	CATCTGATAC	CACTCACCTG	ATTGTTTCTC	ACTCTTCCTC
33101	CACCATTTAC	CCATCTCTTT	AGCTTAATGA	GTCCCCTGTG	TATCTCCCAA
33151	CTAAACAGCG	GCTTACTTGC	CTGTGAAATA	TTCTTCTCTT	GGGTAGTCTG
33201	CTCCCTTCTC	TGTCTACTCA	TGCTTCAAGA	TTCAACATAA	GCCTCTCTA
33251	TGAGGCTTTC	TGCACGTATG	TATATGGATT	TGCTTGTGTA	ATGATTCTTT
33301	CACAGATTTT	ATATTGCTGA	TAAATAAATA	TTGTTTTGAA	TAAGAAACGT
33351	GGTTTTGTAT	TTTTATCTCG	ATTGTAGACT	CCTTGAGACC	AGTACCATGC
33401	TATACAATTA	TTTTTCATCT	ATTATAGTGT	CTGGCATAGG	GACATGCACA
33451	TATTTGGTAC	AGAANNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
33501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
33551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
33601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
33651	NNNNNNNNNN	NNNNNNNNNN	NNNNNTAGAG	AATAAACGGA	ATAAATCCA
33701	ATTAAACAGT	GAAAATATTT	GAGTGATGAT	TTACAGAATT	TTAAAGTCTT
33751	GAGAAAAGTG	AACTCAGTTG	ATGGAAAAGA	GTGAATGTCA	AACTGAGAAC
33801	GTCTATTGTC	CTATGTTAGG	GCATAGAAAG	GCCATTATAG	ATTGAAAAGC
33851	AGTTGTAATG	AATCTTAGGG	TTAAGAAAGA	TCAAGATACA	GAAATATCCT
33901	TGAATTGAAG	TTCCAAAACA	ATGTTGTTTT	GGTTTTTGTT	TCATTTTGAA
33951	TCCTTTCATA	CTTAGGAATA	CCATTTCTAG	TAAAATAAAT	ATTTTATGTT
34001	TAGTTAGAAA	TTTATCTGTA	TTTCATACAT	ACTTAGTACT	TTTGGAATAA
34051	GAAGTGCAT	TTGAAGTATA	TTTGAGGGAA	TGAGTTTGAA	ATTTTGGGTG
34101	CAGGACATTA	TAAAGTTGTA	ACTATGAATA	AATTTCAAGT	ATGCTTATGC
34151	ATAGTTTTAC	CTAGTTTTAT	TTGTCTATTT	GAGTATTGTC	CTTGAATTTA
34201	AAATTTTTTT	CAGCCCCAAC	TGATACACAC	ACATATACAT	ACATAATACA
34251	TGTGTGTGTG	TGTAGCTTAC	AGAGTGTTTA	TAGGAAACTG	ATTTTGTATA
34301	CTTTGGCTAC	TTTGTGTGTA	GTTCTAGTTT	TTTTTCTTTT	ATTATTAAAC
34351	TAGTGCACGA	CATCAATGCT	ATATGATTGG	TGTTTCGTTG	ACCTAGAAAT
34401	AATGCATGCC	ATCTTCTTTT	CACAGCTGTG	TGCCAACCA	GATGCAACCA
34451	TGGTGAATGT	ATCGGGCCAA	ACAAGTGCAA	GTGTCATCCT	GGTTATGCTG
34501	GAAAAACCTG	TAATCAAGGT	AGGAAAACAG	TCTGACATAA	ATACACAATC
34551	GAAGACACCT	CTATCACTCC	CAAATTAAAA	ATATTCTTAT	CTCAAACTAC
34601	TTTCCATGGC	TATTTTTCCT	AAATATGTGA	GCTGCTATTT	TGCTGNNNNN
34651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNTTTTA	TCAAAGGACA
34701	ATTAAACAAA	TTGTATCCTC	TTATTCTCTG	ATACTAATTA	AAATGTATTT
34751	TGAAGAAAAG	AATCCCTGCA	TCAGTAATTT	AGAAGCCTTC	TGGTACTCCT
34801	TGTTTTTCCA	CTAACTAGTT	GGAAATCCTT	GGCCAAATAA	TTAACCACCT
34851	CAGACCCAG	GTACTGCTTC	CCTTTAATGC	CAAAGTCAAG	TAGGGGATTT
34901	GATTTGAAAT	TTGGAGTTTC	CTCCTAATC	TGAGCCCTTC	GATTCTGTAT
34951	TAAATCTCCC	TTCAACTACT	GACCAGTTTG	GAATGTTTCC	ATGATAAATA
35001	AAAATGATTA	ATTTAGCAAG	CACTTTTTTA	AAAAATCAGC	ATCAGTTGTT
35051	TAAAGCAAAT	ATTTATTCAA	CACTCATAGT	GCCCCAGGTA	TTTTATATAT
35101	ATAATCCATT	TTTATCTTTA	CAACAACATT	AGGAAGTAGA	GCATTATTTA
35151	TTATAATNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35301	NNNNNNNNNN	NNNNNNNTTT	GGATAAAAAA	ATATATTTGG	AAATGTGATC
35351	CTCGAACTCA	TGCTACAAAG	TCAGACAAGG	CTTGCTTTGT	TAATTAAATT
35401	CAGTTAAAAA	TTTCCATTAT	TNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NCATTATTAG	GAATTAAACT
35751	AAAGAAAGAT	TAGGGTTAGA	TTTCACTAAA	TAGATAAGTG	TCAAAAATAA
35801	AAAAGATAAG	TCAATTTTTA	CTTATTTTTT	AAATTATACT	CCCTATCATC
35851	TTAAATGTCA	GGTGAAATAA	TCATGGTGTC	TAACATATCC	TTACATACCT
35901	ACTTGACCTC	ATCTGATATA	GAAATGATAT	TGCTGAAATA	CTACTGTTCT
35951	TCAGTGCTCG	ATACTTATTC	CAAGATACTC	CTTGAGGTAT	GTCATGTAAA

FIGURE 3L



REPLACEMENT SHEET

36001	CTAATGATTT	ATAGACACAG	TTTTTTTTTC	ACTATTATN	NNNNNNNNNN
36051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36301	NNNNNNNNNN	NNNGACACC	GTTTTTACAA	TCATCCAGAA	CATTGATTTT
36351	TGAAAACATA	CTCAAAATGG	TGGTTCATGA	ACCATCAGAT	GAAATTATTC
36401	ATGAACCATC	AGATGAAATC	CACACTAGCA	AAAAAGACAT	GTCCCAATGG
36451	TAGAAGCTGC	TATCTCAAAG	TGTGTTCTTG	TATTATCTGC	TATTTGATTT
36501	AGAACTGATT	TTCCCAATGC	TTGTTTCTC	TCTAATACTC	TTTTTAACTT
36551	GAAATTTACC	AAACATACCT	GCATAATCTT	TTTAAATAAG	TGATGCTCTT
36601	ATTATCTCAG	TTTGCTCCTT	AAAAAACTCC	ACTTGATTTT	TCTTCCCCAG
36651	CATAAGTTTG	CAGGTAGCAG	TGTTCTGGTT	ATTGGATGCC	AATGTTTCATC
36701	TTAGAACTCT	AGTATACTTT	TTTTAAAGTG	GTGAACATAA	GCCCTCAGAG
36751	GTTTCTATTAA	TATATCAGCA	CGGTAAAATA	TTGTTGTCCA	AATGTGAGGA
36801	TATAAAATAT	AAAGAAGACG	ATTAAAATAA	GTCACTTTGT	AGATTGCAGA
36851	GAAATTCATT	TAAATTCTCT	TGCAGAAGCT	GCATCAACTT	TAACATGCTT
36901	TAAAGACATG	CTAAAAGTAT	TATTGAAACA	AAAGTTCATC	ACTGGGTAGC
36951	TCCTATTTTC	AGAAAACCG	TTTAACATGT	ACTTTTTTTT	CCTGTAACAC
37001	ATACCTATTT	CTCTAAAGAA	AAAATCGAAT	GTATCAAGTT	AAGATCTTGC
37051	TCCCCAAAAC	CATATTCCCT	AAAGAGAAGA	GGATTGATT	AGTAGCAAAA
37101	TGGGATTTTA	CACCTGCAAA	AATAGTGCTG	ACACTGAAAA	TGTAATTTCA
37151	AGTCCAGTTT	TGAAAATAAA	ACTACAGCTT	AAAATAAACT	TAGGTGTTTT
37201	AATCATCTCT	TATTTTGCCC	TCCTCACAAA	AAAGCAGTGT	GGCAGGTTCC
37251	TGATGGCAAG	GTTNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
37301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
37351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NAGTTTCATC	TAATGGTTCT
37401	TAGTCTGAA	CACCTGGGAA	GCTTGAAAGG	GTTCCACCAG	TTCTTGGTAC
37451	AGCATCTTAG	AGAGTCTCTG	CATCCATAGA	CTTGAGGGCC	CTGTCAGGAT
37501	CAGGGAAGCT	GCCATGTGTG	GCCTGGTTGA	GTGTGAGAGC	TGCCTAGAGA
37551	CTTCCATAAA	AGTTGTTAGA	GAAAAATGTT	GATAGTGCCT	ACATAGCAGA
37601	TTAACTTAAA	CTGTTTTCAT	TCAGGCCAC	ACATTTTAAT	AAAGTAGAAA
37651	ATATGCTTCA	CAGATAAGGG	AAATCAAACA	GGCTCCTTTT	TTCTGGAGGA
37701	GAGAAATGTC	AAAAAGAATT	AAATTGAAA	TAACTTTACA	GAAC TGAGAA
37751	TTAGCTTTTG	ATTAAAAGTA	GCTTTTGGTA	TATGACAGGT	ATTCACTGAG
37801	AATTTTGTAG	CGAGTTATAT	ACTTTAAGAA	ATAACCCCA	GAAACTTGCA
37851	TCATGGTGTA	AACAGCTTGA	ATAACAAGT	GCTTAACCAG	TGCCTTTAGA
37901	GCTGCCTGGG	AAACAGCCAG	AATACCAGGG	CAAGCTGCAT	TTTGGAAC TG
37951	GTTTAAATTA	GTAGCCTTGC	CACAGGCTTA	GTGTGATCTG	CTTTTGGTGG
38001	CTTGATCTTC	CCCCTAAGT	CATTTTCTGG	ATTTGTTACA	CCTAGAACTG
38051	TTAGGAAATT	ACAGCCTTGG	GCTGATCATT	AACATACTGT	ACTCTACAAG
38101	GCACACGTTA	CCTTTCAAAG	CAGATGAAAT	TCTAACCTGA	ATTCTGGCAA
38151	GATTCTTTGA	TCATTTGCTT	CCTTTACTTT	TACTTTTATT	TATGCATATT
38201	TCCCTCCTCC	TTGAGTTTCT	GTACCAACAC	AAACCTCTTT	TTCCCCCAGC
38251	CAGNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NTTTTCCATT
38301	GGGGAATGAT	TTTTAGTATG	TAAATATATC	ACTGCATATT	CTCAGAAATG
38351	AAAGACATTC	TTAGGAATTT	ACAGTGACT	TTATAATAAT	TTCAGAAGAA
38401	AATATTTATA	AATGTCAATT	CCTAATGTTT	TAGCATGGTT	TATGTTTCAT
38451	ATGTTGAATT	CTTTATCATA	AGGAAAGAAT	TGGAGTCTTT	TAGGTCAGAA
38501	CCAGATACTA	ATTTTGTTGA	CTAGTTACAT	CTGAAAGTTG	ACTGCTTTGC
38551	TAAGCACAAA	AATCTAAGGG	CTTTAACTCT	AATATTAAGG	TGGTTACCTA
38601	CAGCCGTAGG	TTTGTGAAAG	TGTATGGTTC	CNNNNNNNNN	NNNNNNNNNN
38651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNGAAG	TTGTATGCTT
38951	TCAACTCCAA	AAACCAATGT	TCATTTGATT	TGGACATTTA	ACTGCTATT

FIGURE 3M



REPLACEMENT SHEET

39001 AATAACATAA TGGTGTGAA ACAGAACGTG ATTGTTAAGT CTCAACTCTC
39051 TTCTTTGAGT CTCACCCATC TTATATTTTG GTAAGCTAAT AATGGCAACA
39101 GTTAACATTT TTTTGCATAA AGCTTCTCAT GTATGTTCCA GAAGCATAAT
39151 TTCTTACATT TAAATGATAA TATTGACGAT CTATTATGCT GTTATTTAAA
39201 TAAAACTTT ATGTAAATCA TACATTGTG CATAATTTTG GAGTATTTTA
39251 AACTACTATT GTACACGTG ATAGTGTAGG GAAAAAATC TTAAGTTGGT
39301 CGTTTACAAT TCAGTGTCCCT TAAATAGAGC AGGTGGATTA TAATCAATAT
39351 TTGTATAATT TGTTTTTTGT TTTCTTCCTT CTGTGTATGA CTAAATAATA
39401 CTTTTAAAAA TGATGATCTC TTGTTTGGAA TTTTTTAAAA AATTGTATGA
39451 CGATGGATTG TTCATTATA ATGTGTGTGT TGTCTTGGG AAACAAGATG
39501 ACAGTGATAC ATTTTAAAGA AAATTAAAGG AAAAGAGAAA CCAGAAAGAAC
39551 CAGAACTAT TGTTTATAAA GTATCTAATG CATTCTTTTT AACTCTACC
39601 AACTGTATGT AATTGTTTAA TATATACTTG CAAAGATTTT TAGGCTAAA
39651 ATTGACATCA GTTCAAAGT GACTCTTATT ACCTTCTTCC TGGTGTGAAG
39701 ACAGACATC CCCAGCTCCT CTTGACCAAG GCAGTGAACA GCCTCTTTTC
39751 CAACCCCTGG ATACCAAGC CACAAGTTTG CCTTCAAGGG GTGAGCGTGC
39801 ATTGTCCCAG GTGGTCTGCT CTTCACCT GCATGGCTTC CTGCAGTTAT
39851 GTCACTCTT GCAATGTTT TGAAGACTAG CCCAGGAGTG TCCAGCCTTC
39901 AGCCCTGAGC ATGAGCAAGC AGCAGGAATT GCCACCTGGT GCTGATTCTC
39951 TGTGCTCTGA AAAGCATGGA GCCCTACTGT CCTTTAATG CATCGAGTAT
40001 CATTGCTTTT CTTTCTCTTT TCTGAATTTT GAAATATGTT CTAAAAACAG
40051 ATAGCAAAAC AACTTTTTC ATATGTAGGC AAATTCAGGA GTTCCAAAGC
40101 AACTGAAATT GGGGGTTTGA TGCCTTTTGC CAAGGAGATT TTAGAAATCA
40151 AGTCCCTTTC CCCACTCTTG AGGTATAGAG TTTTAGGTTA TCTGAAATC
40201 AAAGCATACA TTAGTGACCT TCTTTTGGTA TACATTGTGT AACATCAGAT
40251 AGCCTAAGTT CTGGTTCCTA GAGAGCACTT AGTTGCTATT TGATTATAAG
40301 CAAGTCATTA ACCAATCAGT AACAGGGAGA CAGTAATTCC TGCCCTATTT
40351 GCCTGTGGGG TTGGCGTGAG AATAGAAACA CAAAAATAT TAATGTCTTC
40401 GTCATGCTGG AAAGCTTTGT AGGAAAATAA TGTGGTAGCA TAATTTTACA
40451 GTTCTCTTT TAGGTCAATT TATCTCTAAC CCATTCATAG GTTTAAGAAC
40501 TTAGAATAAC TGAATTAAA TAGTTGAAAT TATTAATCAT TGTCTCTGCT
40551 GAGAAGAAAT TTGATGCATT TGTATATTTT CTACACAAGG AATTAGGGCA
40601 AAAGAAATTA TTTCCGTCCN NNNNNNNNNN NNNNNNNNNN NNNNNGTAGT
40651 TGACATATTG ACATCTGTTT GCCTATGACA TTGCCCCGATT TAAGCACCAA
40701 AGCGGGGAGA AAGTCCAAAT GTGTTAAAAC AAATGAAAGT TTATTTTAA
40751 AAAATCCAGT AAGTTAGTTA TCTCCCGATT TTTCAAGCTA CTTTTCAGTG
40801 TCTGCATGCT AATAAAATTT CTGATTTTTT TCCTGAAGTT TAATAATAAT
40851 GCTGTGCAGC TTGCATTTCC ATTCTGGACC AGTTCCTTC TCCCTCTCCT
40901 TCTCCCATCC AAGCTCCTGA ATCCACCAAC CTACTGAAAT GTATTCTGA
40951 CAATAGTAGA TGCACCTTAA GACTTGTATA CATAATAACT GAAGCATTTG
41001 AATGTAAGTG GTTTATGTGA AAGTTCTATC CTTTAGTGTA AGATAAGCAC
41051 ATGAAATAAT TGTAAATTT TTTTATTTTC CTATTTTATA GATTTTCCTT
41101 ATATATATTA TAAACCTCCA GAGAAAAAGG AAGATAAGTA AATTTAAAAT
41151 AAAACACCA AAGTTTTATT TCTAGGTTCT TTTATCAACT TTTAAGATTT
41201 ATTTGAGACA GTATGATCAA TGACTTCATT TTGTTCTGCT TATTATTGTA
41251 GGAGTATTTA CTATAATTTG GAAGTAATTT ATTTTGAAT TTATTGCTTA
41301 ATTGAATGAT CTCCAATAGA TTGTGATAAT GAACACAGCA TTTATAGAAA
41351 GCAGCACATA TTAACCTACT TAATATGGCA CTAGGTCAAT GAGAAAAGAA
41401 GGTAACATAA TTGAAGACAA GAAACTCTTA AGAAAACTGA GGACAAAAAG
41451 GCTTCTCACC AGGACACCAG ATGCATTTAA TCTTTTGAAG CTCTGTACTT
41501 TAGGAAAAGT CTGATATTTG GCAAAATTTG ATAAACATGG ATGACTATGG
41551 AATCCTATTT TATAGTATCT GAAGTGGCTT TCATAAGGGT CATTGTGAAG
41601 TTTTATAGGAG ACACCTGCCT GTGGCAGATG GGACAAATGAT GGCAGTCACT
41651 AGTGATATTA ACACAGTCA GCTGTCAGGG AATATCATCC AGACCATCAG
41701 CAGCTGGTAG AGTACAGCTT TCTCAATTGC TTTCCATGTT TTGGATACCT
41751 ATATGCCCCG TAATAACAGG TAAAATAGCC AGTACATCAT TTCCACATTT
41801 ACCCATTGAA TGTTGCATGT TTTCTTCCTT TCACATATTC ATACAGTCCA
41851 GATTTTTTTT TGGACTCATG ACAGCACATT GGCTTTTCTT TCCTTTCAGT
41901 TTCATGATTC TTAACCCCAA AGTGCTTTTG CCATGGGAAC GGAAGGATAA
41951 ATTTCCGTTG AAGCATTAAT CTAAAACCA CAGCAGCTCC AGTCCAGATT

FIGURE 3N



REPLACEMENT SHEET

42001	ATGAATACTA	CCATAGCAAT	CCTAAGGGGC	CCTTTATTGG	CCCAGACTGG
42051	AGCCAAATTG	TAGAAGAGCT	GCCCCAACTG	GGCTTCAGGT	TTAGTTCAGG
42101	GACATAGTGT	CTGAAGAAAT	TTCCATCAGC	ATAAATACTC	CTTGTTTATG
42151	AGCTGCCTGA	AACTGTAAAC	ACCGAATCCA	TTCCCATCAG	GAACTCACAA
42201	AAGTTTCTGT	TATGCTTTGA	AAATAAACCT	AGGGATACTT	AACTGACATG
42251	TAAAGAAAAA	TCCATCAGTA	TCCTTTTCTC	GAGATATAGG	TTTTGATTTT
42301	ACTGTGTTAT	GTGTGGTTT	TGTTCTGTTT	TTGTTTAGTG	CAGAAAAATA
42351	CTTAAACAC	AAAGCCTTTC	TCTAACACCA	TATTTGGTTT	TAAATGCTAT
42401	TTGCTATAAT	ATCAAGAAGA	TTTATCAAAG	ACAGGTGTGA	CTCTGCAGGA
42451	CCATATTAGG	AACAGTCATT	AACTCCTCTT	AGAAGATGAG	AAAAGTTTCC
42501	CTCTCATTTT	TAGTAAATTC	TGAAATACAA	AGTAGAAGAA	TATGGGAAGG
42551	GTAGAAATTT	TCTCAGTCAT	TCCTCCTTGA	TTTTTGCTTC	AATTAACAGA
42601	GGGAGAAAAC	ATTTTGTGATA	CTGTAATCTG	CATGGCGCTT	TCGTGAGGGA
42651	AATTTTTTTT	GAAATATTTA	AAATGTGATT	TTGTTTTAAA	AACCCTTAAC
42701	TAGTCAAGAG	ACAATAAAGT	AGAAAATTGA	AGAACGCATA	GGAGATGACA
42751	AAAGTATTTG	GTTTATTTAT	TTAACCTTTC	CGGGATTGTC	CCAGCTCGGG
42801	GTCTGCTTAC	AGTTGCATTC	AGGGCAGATA	AAAGACCTAC	TTGGAAAAATC
42851	AGTAAGATAT	GAAAAATTTT	TTAGATGTAA	TAATTATTTG	GTGGTTTTAA
42901	AACATAATGG	AACTTGATGA	TTTAGTTAAA	TGAAATATAC	AGATTCTTAA
42951	TAAATGAGCA	GATCAGATTG	AAATAGATTA	GATTTGAAAA	CAATTTTTGT
43001	CACTAGACAT	ATTATCTATA	TTTTTTATTC	AATGACATGG	ATTAATAGAT
43051	AATTTAAATTA	TGCTAAATGG	GTACTTATGC	TGGTGGTTCC	AGACAAACAT
43101	GTGGTCACAT	TTCTTTTTTAA	TGAAGCATAT	ATTTTGGGCA	TTACTATTTT
43151	AATGTTTTATT	TGTCATTATG	AGTTTTATGT	TCACTTGAGG	CAGTGTTTAA
43201	TTTAGGTTAA	AACCTTTTCA	TAATGTAAAA	TTTGTTGATT	CATTTCATAT
43251	TGATACTTAA	ACCAATAAAC	CTGAAATACA	TGACAGTCTA	TTACATTTTG
43301	TCCATTAGTG	TTTCCATATG	CCTTTTTTAA	CTGCCGAATA	AATGAAAAATA
43351	TGTTGGTAGG	TTTTTTAAAG	TTCAATTTTG	GACTTGAATG	CATTACTAAA
43401	GTAGGAAACT	GAAGTTTCTT	CTTTAATCTG	AAATCATATA	AAATCTACCA
43451	GATTGAACAA	GAAAAACTAC	AATATTGATC	ACTCTTAATT	TATTTTCGTT
43501	TTATCCTCTG	AAAATATAGC	CTATGTAGCC	TTCTTTGGG	ATGGGAAGGT
43551	CAAAGCAGTC	AAATGTTTTA	AAATCTGTAT	ACTTCTGTGA	AAATAAAATA
43601	TTCTCAAAGT	CCAAGCCTTA	AGGAGGCCAA	TGCCCTTATCC	ATTTAAAGTA
43651	AAATATTCTC	ATGTAATATG	TTCTTTAAAC	AGAGAAAGGA	AGACATTGAA
43701	CGAATAGGGT	TACATTGTCA	GGATTGGATC	TAGCAATAGA	ACCCAAATAT
43751	TTTGAGAATA	TTGGCAAAACA	GTTGTTAGCT	GATAGAGCAT	CTCTGCCCCAT
43801	GAGGACGTTA	GTATGCTGCT	GTTTCTAGGG	TTGATAAGGT	AGGCACCTGT
43851	TGTTGAGAAT	TTTCCTAACT	GGCCTTTATA	AACAGAGATC	CATAAAGGTC
43901	ATGGCGACTC	CTGGTTGCCC	CTAGTGTAAC	GTACCTTCAA	ATTAATATTG
43951	CATGAACAGG	ATCTATCTCT	TATGTAAATG	ACAGTTACTG	TAGCTTGACC
44001	TATTTTCTCT	TTTCAATTTT	TAATATAGAA	AAGAATTTTA	GATGGCTTAC
44051	ATTAGTGCTG	AGGTTTGTGA	ATTTTCTGCT	TTCAACCCAC	ATTGTTTTC
44101	GATCTAAATG	AGTGTGGCCT	GAAGCCCCGG	CCCTGTAAGC	ACAGGTGCAT
44151	GAACACTTAC	GGCAGCTACA	AGTGCTACTG	TCTCAACGGA	TATATGCTCA
44201	TGCCGGATGG	TTCTGCTCA	AGTATGTCAA	GAATCTTAAC	TGTTTTATAA
44251	GTGCTTTGGG	CTTGTTTCTG	TTGTGCTCTG	AGAGCTTGCT	TTTGTGAAAA
44301	TGGCCTCCGG	GGTTCCTCTA	AACAAGATGT	GTGCGTGTGT	TTTACTTTT
44351	GCCTGAGGAA	TTGAAAATCA	AAATAAGAGG	CACCATTTTC	GATGTATAAT
44401	ACTCTTCTAT	CACGGGTGCC	AATATTAAAT	TGATTAGGAA	ATGGTGTTTA
44451	GAATAAGAAT	TACAAAACCTA	AGTATGTTTT	CTAATTTTTT	TTTTAAACAT
44501	GTTTACCCAT	GTCTTCTATC	TGGGCATAGA	AGAATGATTC	CAGGCTAAAA
44551	AAAAAATAAA	AAGAACACTA	CTGACTATTT	AGGGACTGCT	CAGACAGAAT
44601	CCATCAGGTC	TGTTTTGTAA	TTTTAAATCA	TTCATAAATA	TTTTCTTCAT
44651	TTTTATATTT	CATTATAAAA	GCCTTTAGGC	TTTTATAGAA	TTTTAGACTC
44701	TAATAAATAGT	CTAAGACTTC	TAAAAAACAA	TTTCAAATAA	AAAAATAATG
44751	AATATGATAC	CAGAAAAGTA	GGATTCATGT	TTATAAGGAA	GAAATGCATG
44801	TTTTACCACAT	CATTTGGATG	TAAAAAATGG	ACTTTGCCCT	AAAAATCTCT
44851	ATAGGCTGAC	TCCTGAATTG	TGGTATTCAT	ATGATATCTG	ACAATTAATG
44901	ACTTGATTTT	TATTTTFACT	GAATTATCAT	TTAACTGAGT	TGCATAAAAT
44951	AAAGTTAGCT	AATTTTATTT	AACATTGCAT	AAGTATAGCA	TGGAACTTTT

FIGURE 30

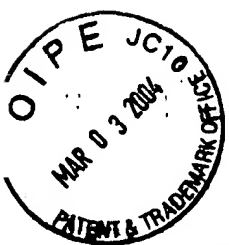
REPLACEMENT SHEET



REPLACEMENT SHEET

48001	GAGTCCTCCC	TGAGAATTG	CTTTTGTTAA	AATTAGAAAT	CATGTTTGCC
48051	ATTAGCGTTA	GATTTTGATG	GTGGGATAAT	CTGGATATAT	TCTACATTTT
48101	TTTCCCTCTG	TTTTATGCCT	CCTAACTCTG	CTATTAAAAA	ATCATTCCCN
48151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
48201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
48251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
48301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
48351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
48401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
48451	NNNNNNCCAT	TCCCATATTT	ATTTCCCTCTA	CATTCAGAAC	TGTTTGTCTT
48501	TTAAAAATTTT	TATAAGTTT	ATTTGGAGTA	GTGGTTATGT	AATAGATAAA
48551	CATGAAAAAA	ACCCAAAAGT	CATAATTTAA	CATACATTTT	ATGTAACAGA
48601	AGATAATTTT	TTAAATTTCC	TCCGTAAAAAT	ATTTACTGAA	AACCATGGTG
48651	CATAAAATCA	TGAGGATTAA	AGGGTTTTTA	AAGAGTCATG	TAGTCATTCC
48701	CAGTCTGGAA	TGTATCATTC	AGGCAGATTA	AATATTGATT	CTTTTGTATG
48751	AAGATTATCA	AGGAAAAAGA	TTTCACAGAT	GATCTTTGCA	ACCTCTGAAA
48801	ATGTCTATTT	AAAAGCAGTT	GTATCTATCA	GTAAAGGGAA	ATAAAAACCG
48851	ACCATAAAAC	AATATGTAGA	ACATTTACTC	AAGCTGTATT	TATGCAAATT
48901	GAATTTATAT	AAAGTGTGGA	TAAGAAAAGT	ATTTGTCTTT	AGACAATTCT
48951	GAACACAATT	TTATAATATA	CACGTAGCAT	AGGGATACAA	CGTAGATTCT
49001	AACATATGAT	TTGCTTATAT	TAAAAAACT	TAGANNNNNN	NNNNNNNNNN
49051	NNNNTCTGTC	AGTGTAATGC	TTCACTTTT	AGGGAGGAAT	GGTTACATAC
49101	TGATTTAAGT	CTTTGACTCT	TTCAGTATAT	CCCAAAAGTT	ATGATTGAAC
49151	CTTCAGGTCC	AATTCATGTA	CCAAAGGGAA	ATGGTACCAT	TTTAAAGGGT
49201	GACACAGGAA	ATAATAATTG	GATTCCTGAT	GTTGGAAGTA	CTTGGTGGCC
49251	TCCGAAGACA	CCATATATTC	CTCCTATCAT	TACCAACAGG	CCTACTTCTA
49301	AGCCAACAAC	AAGACCTACA	CCAAAGCCAA	CACCAATTCC	TACTCCACCA
49351	CCACCACCAC	CCCTGCCAAC	AGAGCTCAGA	ACACCTCTAC	CACCTACAAC
49401	CCCAGAAAGG	CCAACCACCG	GACTGACAAC	TATAGCACCA	GCTGCCAGTA
49451	CACCTCCAGG	AGGGATTACA	GTTGACAACA	GGGTACAGAC	AGACCCCTCAG
49501	AAACCCAGAG	GAGATGTGTT	CAGTAAGTCT	AATAAATGTT	AGCACATTTT
49551	CAATAGGCTC	TTTATAATGA	CTTTTCAACC	ACAGGCCATG	CCTTGAATAA
49601	GAATGAAACT	CGTAAGAAGA	ACTAGCTATG	TAAAGTCGTA	TGTCCTTATT
49651	GACAAATATT	ATAAAGAGCT	ACATAAAGAG	TCAGTCTAAT	TGGGCAAGTA
49701	AGAAAGAATG	TATGTAGCAA	TGGAAGGAAT	ATTCACAAAG	TCATATGGTA
49751	GATGACAGCT	CTTAGCCAGT	ATGGGAATTC	TGACATAGTT	GGATTTACTT
49801	GAAAACCTCT	AGAGGTGGGA	ACTTAACTGT	ATTCCATGCT	ATGTTACTTT
49851	TAATCTAACC	CTTCNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49951	NNNNNNNNNN	NNNNNNNNNG	TGGGAAAGAT	GGTTACTCAG	AAGATACCAG
50001	TGGTAGTATG	TTAGTGAAAG	AGATCTGTGT	AGGACACTAT	GAGAGGAGAA
50051	TGAAGGGATA	CCTCGTCAGT	CTTTGGGTAG	GGAATATTCA	GGGAGGGCTT
50101	CCCGAGTGAA	ACGGAGCAAA	GTGGATGAGG	AAAGGAAGAT	ATTATAGTTA
50151	ACAGGGACAG	CCCAACAAAT	GCAAAGAAGT	AGGAAGCAGT	GTAATAGGCA
50201	GTAGACTGCC	AGTAAATTGG	AGGGTCATGT	CAGGGACAGA	TGAGAGAAGC
50251	TGGACAGCTA	CCCCTTGAT	TGCTGTAAAC	TGATAGTTAG	ACCTACACTG
50301	GGGCTGGATT	AGATCAAAGA	CTCCCAGATT	CTTAGCAGGT	GACTIONGTA
50351	AGGGTAGCAC	CACCAATGGA	GATAGAGGAT	TCAGGAAGAG	AAGCAAGTTC
50401	TGAAGGAGGA	AAAGGTTGTT	AATTTATTAC	CAGACCAAAA	TTTGCATGTT
50451	ATAACTTTCA	TCTGTTCCCT	ATATTTATCT	GCTTGCTCTG	TGTCACCTCG
50501	CTTATTCTTA	ATTACCTTTG	CATTCACTCT	TCCTGTCTCC	TCCTTTATAC
50551	ATTACCAGTT	TGTTTTGTTC	CTTTTCTCAT	TCCTCTATGA	TGAAGCTAAA
50601	GTTTGTGCCT	TTTATATTGA	ATACCTTTAT	AACTTTTTAT	CAGGTGAAAA
50651	AAATACTGAC	ATTTATTATT	CTTTAAAGGG	GAAAANNNNN	NNNNNNNNNN
50701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50801	NNNNNNNNNN	NNNNNNNNNT	ATAAAGGGGA	TATCAGAGCC	GCATTTTGCT
50851	TGTATGTGAC	TCTCAATTAA	ATTTTCTCCT	CTGGGTAAAT	GTCCATTTAA
50901	AGAAAGAGGG	AAATTCCTCT	ATTCTGATAT	AGTCATGTAT	GTTTTGGATA
50951	ATCAATAGTA	TTTTTAGGGG	AATTAGATAG	TAGCTCTCAA	AATATACATT

FIGURE 3Q



REPLACEMENT SHEET

51001	TTATATGTGC	ATAACTATTT	TCTGAAATTT	ATGTTTTTGT	AATTTTCTCC
51051	TCACCCCTC	TCTCCATCTC	AGATACTGTC	TTTTTCTCCC	TATTACTCTC
51101	CTTTTTAAAT	TCTCATCATT	GTGATCATAC	AATGGGATTT	TTAATTTATG
51151	AGTGCTTAAG	TAATTATGGT	ATTTACATTA	TTTTGCTGCC	TTAGGATAAC
51201	AGGGAAATTT	GGCTATTTAA	TGTAAGATGA	TACGCTAAAT	ATTTTTTTCA
51251	TTATGATGAA	AGAATACATC	TTTCTGAGAA	TTTTAAAAAA	TCCTTTCTCT
51301	TTTTAAATG	TTTCTCTTTA	TTTCCAGTAT	TCCTCTCTAT	GCCAATACAT
51351	ATATGAATTA	AAAATGACAT	TGAAGTTCAC	CAATAAAATT	TAGTGCAATA
51401	AAATTGGGGA	AATACAGAGT	TCCAATGATG	TTTGGGAGCA	TTCATTTATAA
51451	GAGAGTGTGA	TCTTAAAGAC	ATGCTCTGGG	AAAGCATTCG	CTTGATCAAA
51501	TGCCAAGGCT	GTTGCATGCC	ACAGATAGCA	TTGCTGCCTT	TAGAAACTCC
51551	TGCCAAAAAT	TAAATTCCAC	TCTCATTTCA	TCTTCAGCGA	TAGCTGCTTA
51601	TTAAGTCTAG	CATGTGTGAG	AATGCTTTAG	ATGCTTTTTG	ACTTGCTGTC
51651	TTGTGGTTAT	AGCATATATT	CTAAATAAGG	CAAAGGCTCT	AAGTTTTTAA
51701	TTCAGGACAA	ATAACCAAGT	TCTATTCACT	GTGAAAACAG	TAAGGAACCT
51751	TAGCACTATT	TCAGTTCAAC	ACCATTCTCT	TACTGAATAT	TTTCTTCACT
51801	TCTGGCATAA	CTTCTTAAAT	CATCCTCATT	CTCCGAGACA	GGTCTGAGAA
51851	TAGAATTTAG	CTCACCTCAT	TTCATAAATT	TTTAGGTGAT	GTAAATTATG
51901	GCCACTATTT	GGCAGTCTCC	TTCAAATAGC	CCTCCACTTT	GTGTTTTTCT
51951	TTACATTGAA	AGATATTTTT	AAATTGANNN	NNNNNNNNNN	NNNNNNNNNN
52001	NNNNNNNNNN	NNNNNNNNNN	AAAGATTCTT	TTTAATGGAA	GAGGTTGTGA
52051	AAGAGAGCTT	TTCCCTATAA	TGTATGTGCG	TTGTTGCCCT	GAGAAAAGAC
52101	TGTAAAGATA	TTCTAAAAGA	AAATCAAGGA	AGAAAAATAT	TATAACAAGA
52151	ACACATCTTC	AGCCCAGACC	TCTCCCCCAA	ACTCTAGACC	TGGATGTCAG
52201	CTGACTGCTT	AACCTATCCA	GTTGGATGAA	AATAGACGTC	TCAAACTCAA
52251	CATGTATAGA	ATTGTTCCCT	TTCTTCCCTT	AAACATCCTC	TACTCTCAGC
52301	CTTCTTATC	CCAGGTAATG	GGACCTCTAT	CACCTGTTGC	TAAGGTCTAA
52351	TAATGTGGAT	TCATCCTTAA	TTACTCTTCA	TACATACAGT	CAATATGTAA
52401	GGAAATCCTG	TTAGCTGTAC	CTTCAAATTA	TATTTAAGTG	TGACCTTTTC
52451	TCACCAACTC	CAGTGCTACC	ACCCTGCCCC	AAGCCATCTC	TCCCCTGGAA
52501	TACAGGCCCA	AAATCCTTTA	TCCAAATAAC	TTATGGAATA	TAGCATTTTT
52551	TAGATTTTAG	AAAATCAGTA	AGGTACACAT	ACTATATAGT	ACACACTGAA
52601	GTAGTGAAAC	ATGCTGATTT	TCCTCTAGTG	CTTTTACTGT	GAACGTATCA
52651	ATGTTAAGGA	AAGGAAAATG	ATATTAACTC	AGAGATGATG	TCTCACAGCA
52701	TATATTACTT	AGCTTGACAA	AATTTTTTTA	TGTTAGCAAG	ATTTAAGGCA
52751	AATTTTTTAC	TTATATTTTA	ATTGGATCCT	ATGATGATTA	TTAAAGAAAA
52801	AAGTAGTTAT	CTCTAGAAAG	TATAAATTGA	GCTCTTGGCA	AATGTGAGCA
52851	AAACCAGAAA	TCAGATTTTT	TTAAAGTTAC	GTGTACATTT	GTCTATAGAG
52901	TTATAATTAA	AAGTATTGTG	CTCATAGCCA	GTCTGTGATC	TGGGGCATAT
52951	TATTATATCT	TCCTATGCCT	TAAAACAATG	TTTCTGTGAA	GTATAAACAA
53001	AGTACCATTG	ACACTGCAGT	TTTTGTCCAT	TTGCTACTTC	CAAAAGAAAG
53051	GGGTACAAAA	CAGAAAAGTT	ATTTAAACTT	TAAGCAGTTG	GTTAGATATG
53101	GTAGTTATAA	TGAGCTTTGG	TATTTTAATA	TGGGGCTTAA	AAATTTTCAT
53151	CTAAACCAAC	ATTAATTATC	TAAGTGTGAT	ATCCTTAGGA	GGTCTTGTGT
53201	AAGTCCCTCC	AATTATATCC	AGCATCTCCA	AAGGTGACTG	AAGTCCCTTC
53251	TAATAACTCA	TCNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

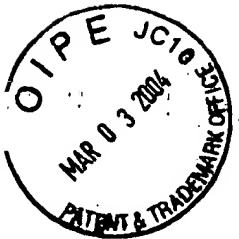
FIGURE 3R



REPLACEMENT SHEET

54001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
54051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
54101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
54151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
54201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
54251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
54301 NNNNNNNNNN NNNNNNNNNN NNTCATCCCA CCACTGGAGC ATTTTTCCTT
54351 ATATTTAACC TAAATTTATG AAACACAGT TTATGCATTT TTAATATTGT
54401 CAGATACTCA GGGTTAAATGG ACACAGTTGT TCATTGTCTC CAGATCCCAT
54451 ACTCCATGTA CTCAAAGACA CTTTCAGGAG ATGACTCACT CTTCCCTGGG
54501 CCCNNNNNNN NNNNNNNNNN NNNNNNTTTC TTAGAAATGC TTTTTCCTCA
54551 CCCACTTAGC AATCTTGTTG ACTGGTCCTT TGAACATTCT TTATTTTCCA
54601 AATCTGTAC ACATGATCGA GTCAAAGATA TATAATAGTC AAATCTGACC
54651 CAATACTGAT CACGGGGGGG TTTCTTTTAA CATGTTTGT AATCTAAATC
54701 ATTTCTCTTT GTTGCAAAGT AGAGATTAT GGGCAGCTAT TTAATCTCCA
54751 GATGTTTCTT CCTCAAANN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
54801 NNNNNNNNNN NNNTGGAATT TTATATTGGA TTTAATTTTT TTCATTCTAA
54851 GTAATCCTTC ATATGCTTAA CTAGCTAAAT TTTACTTGTT GGTCTGATA
54901 TTCTTTCCCC AAATAATCAA AGTTAATTC GATTATGGTT TTTTCTCTTA
54951 TCCTGATACA GCTTAATATA GCCATTGAAA ATATTCTCTA GAAAATCTTA
55001 AGTCTAATAT ACTTCTAAAT TTTAAGCATG AACTGAAAA ATAGTAAAA
55051 GCATAGAAAA GGAATATGAA AATAGCATTG AAACATTGG AATTAAGGGG
55101 TTTTAACCCAC TACTAAAGAT AGAATATACT GAACCAGAAA ACCTAGTCTT
55151 GATTTCCTACC TCTATTTATG AGGTACATGA CTTTGGACTA GTATGAGTNN
55201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
55251 NNNNNNNNNN NNNNNNNNNN NNNNNNTCCC AGCTATCCTT TCTCACTGAG
55301 TAGCTTCAAA GATCAGAGAT AAGGGATCTA GTGTTTGTTGA ATTCTGAGTT
55351 ACTATGAAAT GTAAAAGATT AATGTGTTTT GTTTATCACT GTAAATAACC
55401 TTGATGGGGA GAACCTATGT GATTTAAGGT TGCAACTTTT TTTGTGTGAT
55451 GTGAAATATT AAACATATTT TTAAAATAAN NNNNNNNNNN NNNNNNNNNN
55501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
55551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
55601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
55651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
55701 NNNNNNNNNN NNNNNNNNNN AAAACAATT TTAGCTTGAG GGACCCTAGG
55751 TTTTTTTAGG TTATATGACT AGAAATATAA TAAGATGTAT TTACAGGGCT
55801 AATCCGGTGG GCATGATTTG AGCAACACTA AAGTTATCTG ATGTAGCGTA
55851 AAATTCCTGT TGTTCATTA ATGAGACAGA CTTGTGCTTC TCAAAGGTG
55901 TTTTATAGAG CATTATTTCT CTGAAATATT ACACAGTTGT ATGTGTTAAA
55951 AAGTTCCTAG GTCAAATACA TTTAAGAACT CCTAGGTTTA GCTAAGTTAA
56001 ATAGGTTTCT TAACTGTAG ACTTCTCAAT ACTCCAATGT GCTAACAATA
56051 TTGCAAAATCT CTAAGAGAGG CATATAATGT ATCTTTTCCC AAGTTGTTTT
56101 AACCATGGGA TTATTTGAAT CTTGGGATTA GAGTTTACTG GAATCAACTT
56151 TAGGTCAGGC TGGGCTAAAC TAGGAAGTAT GGAGACCATA CTCCACAAAA
56201 CCCAGTATCC CTCCTAGTGT AGCTCTCGTT GCCTGGTTTT TGAGACTAAT
56251 GGGTTGATCT TAGATTTAGG AATGAGGGTT GGGGAGGGCA GAAAGGTGCT
56301 GCACAACTT AGCCAGAAAA GCAGCCATAA GTGGTGGTAT GCCTGTATGG
56351 ACACCATAGG TTTGCTGCAG GGGATTGTTA AAAAGCCACT TTTCAAAGAC
56401 AAAACTCTGG TTTCACAGGG GTAGGAGCAA TCCCAGGGCA AAGAACTCA
56451 GAAAAACTTT CTGCAGAACC CAAAGTAAAG GAAGTTAGGG GGACATGCTT
56501 TCTGTTCTAG CAATATATAA TGAAATCTTA TATAACTATT AAACATGTTT
56551 TATGGAAAAT ATTTAATAAT TTTGGAAAAT ACCCATGTTA CAAAAATGTT
56601 ACCTGAAAAG TAGAAAGCTG TACCTGCCAT TTGACTCCAA TTAGATATAA
56651 AATACATGTC TGCATATGTC TGGATGTGTG TAAAAGTCTG AAAGAAAAAA
56701 GACCAAAATA GTAACCATGA GTATATCTGT TTTATGATAT TTTGGGCGAT
56751 TTTTCTGTC TTTTGTGTTG CTTTATCCAG TAATTTTAA ACTGTTCAAC
56801 TGTACTATCG TTGATAACAG TAATTCATTA TATCATTAAT TCCTTCAGAG
56851 AAGGGGAGCA GTAAACAGAC CCCACTCTTC TCAGCAGGAA AGTGAGGATT
56901 CTGATCTTAA ATCATGTTTA TTTTATTTTG GACATACTGA GTTTTAAAAA
56951 TTCATTGAAG GTTTATGAG CTTCTATTTT TAACCTTTCA GATTTTCCTT

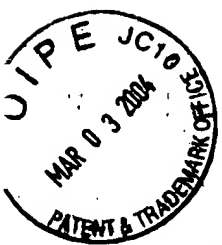
FIGURE 3S



REPLACEMENT SHEET

57001 TACAATTGAA TGTGATAGAT ATGTCCAATT TTAGCTAGGA AATTTGTATT
57051 ACGAGAGGGA ATATAACATC ACTTGGACCA GGAAACAGAT TTTTTCCTCC
57101 CAGTGTGTGC AGAAGCCCAT TTAACTAAA ATAACATAGG ATGTTTATTA
57151 ACTAAATAA CATAGGATGA TTATCTTAAG ATGTAGATTC CTAATCCTTA
57201 TGACACATTT ACTAAATCAG ACTTACTAGG GAAAGTATCT CTCAGTCTTT
57251 ATCNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57451 NNNNNNTCTG AGTAGGCACA CTTAGTCCCC AACACTCAAC CTTTATTCA
57501 ACCAGCGGTG AGCTGGATGT GAACATGACA GACCCAGTAG GGTTCCAATG
57551 CCTGACAACC TGCACCTGTC AGGAAGAGCC CCCTCCTTTC CTGCTCCCCT
57601 GCAACACATG GTTANNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN ATAGCAGGGC TCTTCTAAA
57901 GCATAATGGC AGCTCCAACC CAGCAGAACC ATATTCTGGA TGGAGTCAGA
57951 ACTAGCCAAA TGTAGGCTAT TTAAATATA GCAATTGTGC CTAGGCATGT
58001 GTCCACCTGA CTCATGTAAA ATAAAAAGAA AAGGCGTTAA TAGAAGCCAG
58051 ATTATAGAAC AATATGTTAT TAATATGTAT CAGGTGCTCT TATGAGTGCC
58101 CATATCAGAG AACCAGCCTC ATTGTTGCTG TTATTACGCA ACATGAGACT
58151 GTGCTGCAAT TCCAAGTACC AAGCAGTAAG AAGAAAATTG TTTTCTTTTA
58201 CTGATTGCTG CATGTTGTCC TGAGGTTTTT CCCCTCATCT CTCTCTACA
58251 GATTTTACAG AGTCTGTGGC TAGTTCAGTC ACATTGTTCT TAGTCATGGA
58301 AATATTATGG TCTTCTGAT TCTGTGTAGT GATAAGTAAA AAGATTGTTT
58351 CTGCTGAGGG GTGAAAAGGT CTTCAAAGTA GTTTGCTTTC TTGTAAACAG
58401 TAAGACCTGC AGAGACCCTG AGAAGATGCC TGATATCTCC TTGAAAATTA
58451 AATTTCTGCT AGTGTTTTGA AGGAGCGAAT TGTCACCTCT CACAGGTTAG
58501 GATCTGCTGC TGTGAATTCT GAAAGTTTTC AAGATTTTTC ATTTATATTT
58551 TAATTAGATC CTATGGTAGC TAGTAAAGAA AATATCATTC TCTCCAAAAC
58601 GTATAAATGG GCCCTTGGTG ATTGTGACCA AAGTCAGAAG TCAGATTTTT
58651 TTTTGAAGTT ACATGCACAT TTGTCAATAG AGTTATAATT TACAAGTATT
58701 GTCCTCANNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
58751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
58801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
58851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNCTAC
58901 TATTGATGTT GAATTCATTT ATATAGTAAT GATAACATTT CCTACTTAAT
58951 TCATAAAAAG ACAGCCTATG CTGTTTCTT GTTCTGAGTT TATATGTTTC
59001 TCATGCTTTT TATTATGGTT CATTACAATT TTAATGTTAT TTTTAACTAA
59051 CTAGATCCTT TTGAAACAAA TTGGTTTGCA AGTGTGAGCT GTTAGGTGCA
59101 CAGAGAAAAA TGAAAATAGA AACTTGCGAT TTTATTCTAG GCTTGTTACC
59151 AAATATTTAG AATACTGTGT TTTATTTAGG TGTTTATAGT CTCATTAGAC
59201 AGTTGTGATT TTAAAATAGA GACCACATCA TCTCAACTTC TTTACTGTGA
59251 AAATAATGAC AATAGTCTTT TCAGAGATGA ATCTGTCTAG ATGGGAAATT
59301 TACATGATTG ATCTGATGAG NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59351 NNNNNNNNNN NNNNNNNNNN NNNNNNNAAA ATAATCTGAC AAGTAGTTTC
59401 CCCAGAAAAT CTGATTTAGT AAATGTACCA AAAGGATTTA GAAATCTACA
59451 TCATAAATAA ACATTCTATG TTATTTTAGT TCAGACCCCTA TTTTAATTCA
59501 GACTTCCTAT GGGATAAAAA CTTCCATTCT TTCTTTAAAT AGATTCTTTT
59551 GGCTTGAGTG CATTTACACC TGTCCCAAC AGCTGGTGGG CTTCTGCTCA
59601 CCCTAGACGG TGTTCATGCT GCACTCAGTC CAAGCAGCCC TTATCAGAGA
59651 GTCTTCTTAC CACTTGCATT CTGGTGCAGG GAGCTCATTG CTGGCAGAGC
59701 CTAACCTTCA TGGGAACCAT TGGCTTAGAA GAGAGGAGAA GNNNNNNNNN
59751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNTATCC

FIGURE 3T



REPLACEMENT SHEET

60001 TGTCTCCGGG CAGTGTCTCT GAGTCTTTCT AAAACTTTAT TAAAAGTTCC
60051 TACAATACAT AAAAGAGAAA TAGGTATGTC ACAAAAATG GGCTCATGT
60101 TGATTAGCAA TGCTATGCT CCACCTTTCA CCAGAGATTT AACTTTTTTG
60151 CCAATTTTGC TCTTTACTGT CAGCCCAAAG GTGTCTGTGG AACTTTGTAG
60201 ATTCTTCTTA TGGGATGAAA GCTTTGACAA ACAAGGTCTT ATTTCTGTGA
60251 GTCCAACAAC CCTTTTCTTT TGGCTTATAA TGAATAGATG GCTAAAACCT
60301 TTCTCTAACA TGGTTAAAGA AATTTAGAAA ACTAATTTCC AGCCCTTTTA
60351 TTTGCTTTTC TCTCTGATCA CTTAAAATG TGATGCATAT GTCCTGCATC
60401 TGTNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNCATC
60451 TCATAAAACT CTTGTCTATC ATCCCTACGC TCCAATCTGT GTCTCTAAAA
60501 GCCTCTAGGT TTTGCCACCA GAAACAGCCT TCAGAATATT GGAATAATTA
60551 CATATGTACC ATTCTCTTCA ATGAACATA CTCTAAGCA TAGAAGTAAT
60601 TTAAGACAGT GTTATTTTAA ATCATTAGT CCAACAACAA ATGCCAGAAC
60651 TGGCCTGGGT AATGCCATAG GAACCACCTT GTTCTCTATG AAACAGGAAG
60701 AGAATTTGCA AACCTACCTT TACTAAATA TGCTTACATT TTGCTATAGT
60751 TACTCTTTGGC AAGAAGTTGA GCAGTGGGAG GTGTATATGA TAATATTTAC
60801 ATTTACTTCT CTGTGCTTAC TGTTAATGTT TTCTGGGTAA AAATATGCAA
60851 TTGACTATTT GGGAACTTC ATTTGTGAAC ACAGGTATA TATGATCACA
60901 TCCCTGGGGA AAATACATAT TTAGTAGAAA GTGCCTGGCC AGCATTTCTT
60951 ACAAGAACTT TCCTGCTCCT TTTTGTGGCT GATTTTACCC CTGACTCCAG
61001 GGCCCACTAG CCATTAGAAA GTACTGTGCT CCTCAGCCCA GTCCAACCAT
61051 GCCTTTATCC AGCTTCTACT TGCTTACATA CCTGTACATT CCCTTCTTTT
61101 TAGTTTATGC AGAAGGCTGT AAGAAGCAAC AGGCAAGACA TATCTTTTGG
61151 TGGGTAAAAC ATGGACCAAT GGTATAAAGA TTCTGGGGAC ATTTTCTAAA
61201 AATATATGAA CATTATGGT TGATGTTAAT TTTAGTCATA ATTCCCCTAT
61251 GACACCCACT CTCACCTTCT TCCTGTTCAT TCTCCAAGCT ACTACCAGTA
61301 ATGGTCATTT CAGCATGCAA ACCTGATCTT GGCAATCCTC TGTTAATCCT
61351 TCAGAGCCCG CCAGTTTCCA CCAGGGATA CGTCCAAAAT ATTTACAAGG
61401 CTTTAAAAGC TCCTGCACAC TCTGCTTCTA TCTCCAATTC CATTTGATGC
61451 CCTTCTCCT GCACCTTCTT GCTGCCTCCC TCCCCCTGTA AGGTCTACAG
61501 CAATTCGTAT GTTTCAGTCC CCTCTCTTTT CATTCTCCAG AGCCATAGCT
61551 CATAGTACTT CTTCTTATGT CATAGAGAAA GCATCACTTC TCAGAGATTT
61601 TTATGACGTG TATCCTCCCC AGCCTAGCTT AGCCAGTCCC TCACTCCCCA
61651 CTCCCGTACT CACTAGCATC CTCTGCTTCT TTAAAGCACA CATTACCTGG
61701 GGAAATGTT AAAAATCINN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
61751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
61801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNAATGAGT GGATGGAGTA
61851 GAAGGAGGCA GGATGCATGG ACAGATGGTG GAGGAATGTT ATTGCTAGCA
61901 CTTCTCTGAT TCTTTTCTAG TTTCTAAATT TATACCATTC TAATCTAAG
61951 AATTAATGGT TCAACTGCAG AGAATAGCAG GTATGCATTT GTTTTATGA
62001 AATATATATA TTGTGTATTT AAGTTGAATA TTAGCCCAA GTATCAAGCA
62051 GGGGAAAGAA CAATTAGAAA AATCATGTAC CAATGTCTAT TCCTGGGNNN
62101 NNNNNNNNNN NNNNNNNNTT AATTAACATT TTCTGCATTG ATCAAAATAG
62151 CTCCCTTGAA ATCAAAGAAA AGTGTTTGAA TTTCACAAAC ATATTTCAAT
62201 TTCATAGCCT TGCGTTCAAC AAGTATCAAG CCTATTCTAA GTTCTCTTTG
62251 AGTAACCAAA ATACAAATAA CAGACATATA ATTGCTATTT ATATGTGATC
62301 TAACAGAACC CTCTTTTATT TAGATGTCTT AGGTAAGTTT TTTATTCATA
62351 TTTATATTTT TTCTTTTAC AATCCTAAA ACATAGAATT ACAAATAAAG
62401 TGAACCAATA CAAATGAAAA AAAAAATTTC ATTTCTAATA CTTAGATTAC
62451 CAATATTTAG CATATTTGCA TATTGGTGTA TTTATCCCTC TTTAGTCTT
62501 TTTTTTTGGT TTGTGTTTCT TGTACATGAT TGTGATAATA ACATAATACT
62551 GCTTGAATGA TTTGTTCTGC TACTTATTTT ACTTAATATT TTCACATAAA
62601 CTCTAAAGTG TATCGGGGGT GGGTAGTTTT TTTTCTCTTG AAACCTCAGT
62651 GGGATGCTCT TAGTAATCCC ATACTGGTAT GTGTGAGGAA GGAAATTAG
62701 TTAAATAAAT TGGTATGGTT ATAGAGTAGA GCACACAAAA TTGTAAGAAC
62751 CAATAGCTTC TGAGCACTTC TGGTCTCTAA ATTCCTTGGA ATGTTTCCCA
62801 GTGGATTGTA ATGAAGGTAT ACATGATCAT CTGCTGCTAA ATTAATGGT
62851 TCTTAGAAGC CAAGAACCNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
62901 NNNCATCTGA CATTTTTCAA GTTGTTACTT GACTAATTCT TTGTGTTGCC
62951 ATCTTCTAAC TNNNTTAAAC NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

FIGURE 3U



REPLACEMENT SHEET

63001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
63051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
63101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
63151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
63201	NNNNNNNACA	GGCTCCCGGT	GCCAGGAAAC	CTTTACATCA	ACACTCGATT
63251	TGCCATTGTA	TAGTCCCTTCA	TCTGGGAGGA	AAAAAAAAGA	CGGAGGGGAG
63301	CTTGAAAAAC	TGTCATAATG	TCCCTGGAAT	ATGGTACTTT	TAAGAGTTGA
63351	GCCTATTCCA	TTTTTGAGAT	GATTTATATA	AGTTACAACA	AAAGAAGGGG
63401	ACAAAAACAT	GATTGTCTTA	TGGAGTTTTT	ATAACTTTCT	GTCACAAGAA
63451	AGCACGCTTG	TCTACAATTT	TGTAATATTT	CTAGTAAATA	AAAGAGGCAC
63501	TCCCGCTCTC	AGAGCACCAA	ATAAGGAAAG	TGTAATTGGA	TGTCATTGCT
63551	GTCAGTCAGC	TGGGTATATA	AAGAGAGAGT	GGGGTTGCCT	CATCCCTGGG
63601	GTATCCACAG	TCAGTGTGT	CCCTAGAGCT	TCTTTTCTTT	CATTGCTGCC
63651	CAGCTGGGTA	TATTGCAAGT	ATGGATTATA	AGAGGGGAAG	GGACTTCACT
63701	GTTTTAACGT	TTGAAACAAA	AAGGAAAAAA	CTCAGAAGTA	GTAAGCTAAA
63751	AACAACTTGT	GCAAACGTTT	TGGGATTATT	ACTTAATTTT	AAGAATTTTT
63801	GCTAAAAACA	ATAGGAACAT	CGTTGAAAAA	AGAACCCCTT	TGAGTGATGA
63851	CTGTTTCATA	GTGTCTTACA	TCTCCTACTC	CCTGCCTTAT	AAAAATAAAG
63901	CTAATTAATT	GAAGTTCTGG	CAAAGAGAAG	GGAGTATTC	TTGGCCTTTG
63951	ACCANNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64201	NNNNNNNNNN	NNNNNNNNNN	NNAATGATTT	AAAGAAATCA	ATTATTTTTT
64251	TAAAGTAGAT	TCTTATGCTT	TGTCCCACTT	GTGTCCCTTG	AGGAAAAGTG
64301	TGAAATACTA	CCTGGGGTTC	TAACAGGATC	TTTGNNNNNN	NNNNNNNNNN
64351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNA
64451	CACATGTGTG	TAAATAGCTG	CAATTCCTTA	TGAAAGTGTG	TAATAGGGGC
64501	TTATAAGCAT	GAACCTCTGA	GGTACAAGAG	GGAAGAATTT	GATTCCTGCCT
64551	GGGGCAGAAT	CACTCCACAG	AGGCCGTGAT	ATTTATGCTG	GGCCTTGAAG
64601	GAAGAAGAGA	TTTTTGGCAG	GTAAATTAGC	AGGAAAGAGA	GCATTGGGTC
64651	TGAGACGTGA	AAATGAATGG	CATGTTTGGA	CAGCATTGTG	TATTTTGGTG
64701	GGGTAGATTG	TAAACTCTGG	CCCAAGAAAGT	TTGAGTTTGA	TCTTAAAGGA
64751	GCCAGGGAAA	CTGTTTAAAG	AAGGGAGGCC	ATGGTAGGAA	ATGTATATTA
64801	GAGTGCAACA	ATGTGCGGAG	TTCACCTGGG	GTGGGGAGTA	CATGCTGTGA
64851	TTAGAAACCA	AACCATTCGC	TTCCATCATA	GGTATTTTCA	GTAAAAACAA
64901	CCTTGATTTA	AAGATCATAA	TAATGTATCT	TTCGTAGAGA	TGAACCTTAG
64951	AATTTCATAG	AGATGAATAG	TTGGCTAGAA	ATTGGTTGCT	CTATTAAAAAT
65001	GTATTTTCCA	GATAAGACT	TTTTAAGTTA	TTTTTGTGTA	ATTTTAGAAA
65051	CTTTTGAAAA	TCATTTTAA	AAAATGTACC	CAGATCAAGG	TTGCAGTATA
65101	AATCACTGCA	GAACAAAATT	CGTGAATCTT	CATGTGATAT	ATAATTAAAT
65151	ATTTTGGATT	CATCCAGATG	AATAAAATGA	CTAGGCCTTT	TCCTCTGCCC
65201	CTTGTTAAAG	GTAATGCCCTC	TTTATCAATA	CTTCACACAC	ACACACACAC
65251	AAAACTCAA	AACCTTTCTC	TTGCAGTTCC	ACGGCAACCT	TCAAATGACT
65301	TGTTTGAAT	ATTTGAAATA	GAAAGAGGAG	TCAGTGCAGA	CGATGAAGCA
65351	AAGGATGATC	CAGTGACAC	TTACACTCTT	AGTGCCATCA	TAATGACATT
65401	TTATTGTTTC	TCTCCATGAA	AATAACTTTT	AAATGTAGAT	CGTTTGGACC
65451	ATTTGGGAAA	ATTACACCTG	TTTTCTTTAA	CAACTCAGAT	TTTCTTTGTA
65501	GTAAATCAG	TTGAGCNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
65551	NNNNNNNNNN	TAGTACTTAA	ACTGTAAAAA	GGAAATCATA	TTTTATAAGT
65601	GATGATGTAA	CATTGTTATA	ATTTGGCAAC	ACTTGTGTGT	TCTATTTTAA
65651	CAGATGATGC	ACTATTGTGC	TGAGAAAAAG	TTAATGTAAT	TTCCCTTTGG
65701	TCTTATGGAA	AGAAGCTCTG	GTTATATGGA	TAGGAGAGAA	CACTTGTGT
65751	CTAGATACCC	CTAGTTCATA	GATTCATTGT	TTGTTTTTTG	TTGATTTTCT
65801	GATCCACTCA	TCTTTCTGAT	TATTTCCCTG	TAGGTGTTCT	GGTACACAGT
65851	TGTAATTTTG	ACCATGGACT	TTGTGGATGG	ATCAGGGAGA	AAGACAATGA
65901	CTTGCCTG	GAACCAATCA	GGGACCCAGC	AGGTAAACC	ATTTCAATTA
65951	ACTTTTTCTG	GTACATTTAA	CAATGTGATA	CTATCTGAAG	ACTCCACTGC

FIGURE 3V



REPLACEMENT SHEET

66001	TGCTAATCAA	GTCTACTGTA	ACACATCTCT	GTGTTTACTT	GATAAAGATG
66051	GTCAAAAAGG	ACCATGCCTA	GCATTATAT	TTCATTTCTT	TGAAAGAGTT
66101	AAATTTGTTA	GCTATCAACT	AGCACTATAT	TATGGGAGAC	AAGTAGTTAA
66151	TTAAAAGGTC	AACTAATTTT	TCTCAAAAAG	CTTGATAAAT	AAAATATTTA
66201	GATTAATTCT	TGCAAAATAAT	TCTTAAGTTA	TTTGTAGCAC	CCATTCCCAG
66251	GAATAAAAGA	AGTAATATAG	TGGTATATCA	GCCATGGTAA	TAGGCATTCC
66301	CCAGTTGNMN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNAGAT
66351	TTGAGTGGTA	GTAGAAGAAC	ACAGTGGAAG	TTTCTATAAA	GTTGTGATTA
66401	TCCTCTGAAA	AAATTTCACT	CTAACTTGGG	TGCTGAAGGA	AATGGTTACG
66451	AATCACCACC	ACTCATTTTA	TAACAAAAGG	TAGATTTAGA	CATAGTTCCT
66501	TGGAAGTCAA	AGGAGTTTAA	AATGCACAAA	TTCTTATTAA	TCTAAAGTTT
66551	TAGTACTCAT	AAGACATCTT	TTCTTCTAGA	TTCAAGATAG	CTTTTCTCCC
66601	CTCAGTAGTT	AAATCNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
66651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
66701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
66751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
66801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
66851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
66901	NNNNNNNNNN	NNNNNNNGAAG	TTAAATCTTT	TATGGATAAG	GCCTACTTAA
66951	TGGAAGGGTG	AGGAGTTTGG	TTTCATTTTT	TTTCCTTTTT	ATACTCCTGA
67001	TTCTAGATTT	TAAGAAGATA	CAGAATGTGA	AGGAAAAGCT	TGTTATTTCA
67051	TTTATTTTAA	AAGCCTAGTT	CTTGAATACC	ATACTGGAGA	AGAGCACCAA
67101	ACACAGAAAA	GTAACTTGA	GAGAGCTCAT	GATATCTTAA	ACCAGCTCNN
67151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
67201	NNNNNTCATG	CATTTCTAGC	AGGCTCCCTG	AAGATCTCTA	TGGTGGTCCT
67251	CAACGCACAT	TTTGAGTAAC	AAGGTATTAA	AAAATTAGTN	NNNNNNNNNN
67301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
67351	NNNNNNNNNN	NNNNATTAC	TTAAAAATTA	AAATGTGAAT	TAAATTCCTT
67401	AAAATAGGAA	TATTCATAAA	ATTCCAAATT	GGTTCATACA	TTTCTTTTCA
67451	TTGTAAAAGA	CAATATCATT	TAGTGCCTCA	CACACAGTAC	TCTCAGTCAT
67501	TCTTGCAATTA	CTGTCTTACT	CATTTAAAGT	TAACCTCTGAG	CAGGACAGCA
67551	TTATCATTA	TGTCACAGAT	TCTGTGAATA	AGAGAGAAAC	CAACATATCT
67601	ACNNNNNNNN	NNNNNNNNNN	NNNNNTACAA	TATAAAATAC	CTATGACAGT
67651	CCTAGCTTAT	TTAAATCTC	ATCAATTTTA	TTTAATTGTA	GCAATTAATA
67701	TAAATTTTAT	TCATTGCTAC	AGAGTTGTAG	CAATTTACAC	TCCTACCAAC
67751	AGTATTTGAA	AACCAATCCC	AACAGATATT	ATAAAAGTAT	TTTTTTAAAT
67801	CTCTACCAAT	CTTATAGGTG	AAAAGGAATC	TCTTTTAATT	TTACTTTGCA
67851	TTTCTTCTAT	TGTGAAAAGT	TGATCATGTT	TTATCATCTA	CTCGAGGAGC
67901	AAANNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
67951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
68001	NNNNCTCTGT	ACTACTCATG	CAGGCTCCTA	GACAGTCCAA	TACTCAGAAC
68051	ATCTGCAGCA	TTATTGTGTT	TTTGACTGTA	CCACAGGCTG	GCCTCAGTAG
68101	GTGTGCATGT	GGTAGTGTGC	ATGATCTGAT	TAGCAGATCA	CAGACCTGTA
68151	GATTAGACTG	ACTGACCACT	GACCTGGAGT	AGTTTGCTAC	AGAAGGAGGG
68201	ATCTTTGGCA	GTCATGTATG	ACAGAAATGGT	GAATAATATT	TATGGTCATA
68251	ATGAATGATT	CCTTCAAGTA	AGTTACACTG	GGGAGAGTAA	TTCATGCTAA
68301	ACTCAGGAGA	ATTCAGTGCA	CTTCTATGTA	AACAATCTAT	GTAAATAACT
68351	TGAGTTTTAG	AATTTAAATA	CTGTATTTTA	GAACCAATTT	AGTCCTTTTC
68401	AACATTTTTT	TATTATTCAT	TATATTGTA	AATGTTTAAA	TTTGTGTGTA
68451	CCCAAATCTC	CCTTCTCTC	TGATGGAAAA	ATGAGAAGAG	GGTTAGAAAT
68501	TAGAATGGTA	GACAAAGAAA	TTTGAAATCG	TTATTGGACC	GTGTTAGTAC
68551	AGAGCAAATT	GAAAGGAAGA	GATGCCTGCT	TGAGTGATTG	GATAACTCGT
68601	GATGATTGGC	TACGGTCCCT	GGAGGATGCT	TTTCTAGAAT	TGGTCCAAGT
68651	TTTTACCAAG	AACCTAGATA	AATAGGACAT	TGAACCTAAT	ATTGAAGATA
68701	AACTGACCAA	ACTACGGTTG	ACTCAAATCT	GGAGAGGAAA	GTGACTATGT
68751	GTGCTGATAC	AACCAGCATT	CGAAAAATTA	GATTAATGGG	TCACAATTAA
68801	GAAGGTGAAA	TGTAATGGGG	TTGAGTCGAA	GTTATGGCTC	ATAGTCGAGA
68851	AACCAGTCAC	ACATCTGAGT	GAGGGGGAAG	ACCTGACATA	TCACTAAGGG
68901	TAGAAGACTT	TAGAGTTTAA	GTGTGTAATG	AAATCAATCT	AAGCGAACCT
68951	TGTGATGTTG	CTGCCAGAAA	TATGGACCAT	CTCTATAGAA	ATATGCTATG

FIGURE 3W



REPLACEMENT SHEET

69001	TTTCAAGAAT	GAAATCCAC	TTTGGTTAAG	TGGTGAATCC	ACTTTTGAGA
69051	ATTC'TTTTT	TCTAATATGA	GAAGAATAGA	GTTGGTCACT	TAGAAGAGGA
69101	TGACCTGCAT	GGAAAGGTAT	CTCCAAGCTT	GTGAAAAACA	GGCAAAGGAA
69151	CCATAACGTT	TAGCCTGGAG	AAGAAATGAT	GCATCAGGGT	TCCTTTTCAA
69201	ATAATGACT	AGGGTTAGAG	TTGTTCTCTG	TGACCGAAAG	GGGATGAGAA
69251	TAGGATTGAT	GGGTAAAAAA	TACAGGGAGA	TTCATTTTGG	CTCACTGTCA
69301	TCTAAAAAGA	GAACAGGCTG	ACATGGAAAG	AGTGAGTTAT	CTTGGTGGAA
69351	GCATTTGACT	GGGTGACATA	TGGCAAGATA	CTGTAAAAAG	GTTT'TGAGCA
69401	TCAGATGAAA	GTTGGATTAG	AAAACCTCTA	AACCAGCTCT	GAGAGCCTGA
69451	TTCAGAATGG	AATGTGGAAA	TAGTCCCAAG	AAATTCAGTG	AGCAGGATTC
69501	TAGCTTGGAA	AGAAGGATGG	GAAGACCAA	AGATGGCAGA	GAGTTGGAAG
69551	GCAGGATATG	TGAGGATGGA	ATTGCAGAAT	ATATTTT'TAG	AATATGTTGA
69601	GAGAATTATA	ACCCAGCACT	GATGGGAAAA	TACTAATAAA	GCTTACCTTT
69651	TCATGGT'TTT	TTAT'TCTAGG	AAATTCAGGT	GGATGGANNN	NNNNNNNNNN
69701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNTC
69751	ACATGTGAAG	GCCAGAGAAG	AATATAAAAA	ATC'NNNNNNNN	NNNNNNNNNN
69801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
69851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
69901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
69951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
70001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
70051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	AATAA'TTCT	GTGTATTATT
70101	CTAATTACCA	AGCTAATTAT	TTACCTATTT	CTATCTAGAT	TATACCACTT
70151	ATAAAGAAT	ATGTGTTTGG	ATATCCAATT	ATGGATGATT	TTAATGATGT
70201	GCAGTTCTAA	TCCAAGATCC	AGATTTGTAA	ATATTCTTAT	ATGCTAATAT
70251	TTCTAAGAAA	ACTCTCAAAA	CTCAAAACCT	TAAGAAATAG	CTGCAAAATA
70301	AGTGCAATTG	CTAGCTGCCT	TTCATGGTGC	TATTAGGTTT	TATCACATTC
70351	AGTCACAGTG	AGATGTGAAA	TTACAATGC	CTCTAAGAAA	TGGAAAATTG
70401	TGCTGCTGAC	AGACATGGTG	ATGCGCTGCA	GGTATGTAGC	TGTGGCCCTG
70451	GGGACACACC	CTTCTCCTGT	GTGTGTCAAA	GCTAGAACTA	AGGCCCTTTT
70501	CCTGGAACCT	TGATCTCTGG	AGAACAAGGA	TTAAGGGCAA	CTGACTCAGC
70551	ACTCTGTCTG	CCACTGATAG	CTACAAGGAA	TTTGC'TTACA	TATGTATCAA
70601	GTATGCCAGC	ATGTACATAC	AAGTATGTCT	ATTT'CAGCAT	TAAAACATTA
70651	TTTTAAATA	CACATAAATG	TAAAATAAAT	CAACAATATA	AGTGAAAGCT
70701	TTCTACCACC	CCTGACTCCC	CATTCAACCAC	CCAGCAAGAT	GCAGCCAGTT
70751	TCTTGATTAT	GTTCTCAGAG	AGATATTTT	GGATACAATG	GCATTCTCTT
70801	CTGTGCCTTG	CCTTTGTCAC	TTATCGATAC	TACCTTAAGA	GTTAACAGGN
70851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
70901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNTGGGG	ATAATAAGTA
70951	CTATCCACTA	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNGC	TGAAGCATGT	CCCCGTGTCAG
71051	TACATACAGA	ACACCNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNTCAT
71501	TTTTTCTCTG	ATGTTCTTTA	TTTTTCTTTA	GTATTTT'TAT	TGATTTATGG
71551	AAGTTT'TCTA	TACAAAAAGA	AAAATTATCC	TTTTTTAATT	TGTTGCAAAAT
71601	ATTTAAAAAC	ATTTTGT'TT	GTCTATTTTA	TGGTATTTT	ATCTTAACAT
71651	GCAAA'TTGG	AAACTTAAAT	GTTCTTCAGT	AAGAAATTGG	CTAAATGGTT
71701	ATTGGCATA	TTGCAGCAAT	GCAAAAGTGA	TTTGCTACCA	TAGAAAAATG
71751	GTTATACAAG	AAGCAACTTA	CAACACTGCA	AATATAGTAT	TCCTTTTTTT
71801	AAAAAAGTT	CATATTCATG	TGCATTTATG	TGAATGTATT	ACATAAGAAA
71851	AGTTCAGAAG	TCAAAACCTT	CACAAATACC	TCTAGATTTT	GTGAATTGAA
71901	AATTTAAAGG	CACCAACCAC	TACAGAATTA	AAAATAAATA	AACTAACATT
71951	TTATAACCCA	ACTTCTGGT	CAAGTTT'TGC	AGCATCTATT	ATTTACCCTC

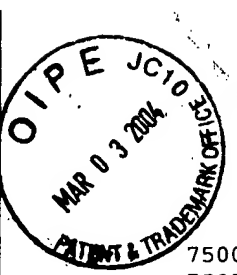
FIGURE 3X



REPLACEMENT SHEET

72001	CCTCCCCAAA	ATTCTTGAGA	TATTGTGATA	CTGTAAACTG	AATGAATGTT
72051	TAATAATAATT	GTACATTTAT	CACCAGAATT	ATGAAATCAG	AAGTGAAAAAT
72101	TTTAATAGGT	AACCTGCTTG	ACACTGAATC	AATTTTTCCT	TTAGTTAATG
72151	TTCCAACCTG	TATCATTTCC	TTTATTACAA	AGGGAACGAA	TTCTTCATGG
72201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
72251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
72301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
72351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
72401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNTAC
72451	CTGTGATGAT	TCAAAGCTG	ACTTATAGTG	AGACATGTAA	ATATTTTGGC
72501	CCAAAATATT	GTTTGGATTA	GTTTGTGGAG	GAAGGGGACA	AGGGAAGTGG
72551	GAGAAAGATT	CTTAAGACAT	TATGTATTTT	TAGTGATTCA	AGTACGTGAA
72601	TCAAGGATCT	ATTTCCCTGC	AGTTTTCCTG	TGTATCCTTG	GAACATCATT
72651	CGTTGATTCA	AACATCCTTA	AACACCTGCT	GCCTGCTAGC	AGGGTAACAC
72701	AGAGGTTTGG	GGGAACTTT	GGTTCAGACT	TTTAAGTTGT	TCACAACCTG
72751	CTGGGGAGCC	CTTAGCACAG	AGGCTGGCAC	ACAGTAAGTG	CACAGAAATC
72801	ACCTGTGACC	TATAGAGCTC	CGACGGGACT	TGTTAGAGAA	GACACTGGAA
72851	TAAAAAGTTA	ATACCAAATT	TTATCATGTC	CTGTATAAAT	TAAGCATAAG
72901	AAAGAGATGA	TAGTTTATAT	CTGTAACTG	AAAACATAAT	GGGATTACTA
72951	CCAAAATAGA	TACACATGTT	CAACATTCCA	ACCATTTCCT	TATGGAAAAA
73001	CCAGTGTGTA	AACATACACT	GTGTTTTCAG	TTGACTGAGA	TAAAAAGGCC
73051	TGAGGGAATG	TCATTTGTAT	ATGGATCAAG	TTTCAAAATA	CTACTTGCAA
73101	CTTTCTCTCT	CTTGAGAAGC	AGCACCCCCC	ACTTCACTGC	TGCTTAACCA
73151	TTTTTTTTTCT	AATGCAGTTT	CCTTAACAAC	AGAGGGAAGA	AAACTCTGTA
73201	GCCCTAGGGA	TCTGAGAACA	TCATCAAAGT	GGTCTATCTA	AAGTGAAAGT
73251	TTTTATTAAT	ATTTGTGTTT	ATGTATATAT	AATAGGACAT	ATTTATAGAA
73301	TAGATATGAT	ATAGATTTGT	TTTACTATAA	AAATGTTTTA	AATGGCTTAC
73351	CTCCAAATAA	AATGAAGCT	CCAGGAAGAC	GGGGAGGGTT	TCCTGAATAC
73401	CTCTGTATCT	TCCTGGTGTT	AGATTACAC	CAGTGTGAGA	AGCTCTGCCA
73451	ACTCTGATTT	TTTTTTTAAA	GAACCTTTAC	GTTTAGAGAT	TTTTTTTTTT
73501	TAAGTTGGGG	GAGGAGAGAA	TAAGCAGATA	TAGGGCCCTT	TAAATCACCA
73551	TCTGCTTTAC	TGTTCAGAGG	TTAATTATCC	ACCAGAAAAT	TCTCCCTAGA
73601	AATTTAGGGT	CAGTTTACC	AAACCACCAA	GCCAGATCGC	CAGGGGTGTT
73651	GGACAACGTT	ATCATAAACT	GGTGAGGGTC	ACAAGGTGGT	GAATGTGTAT
73701	ATGTTGTCGT	ATGCCATAT	GTCTGATCAT	ATTCCATTGG	AAATATTCAT
73751	AGTGTTTGGT	TACTAATTAT	TGTGTGTCTC	TGGCATTACT	TGTACTTTCC
73801	ATGAGCAAAG	TAAGTGAATG	TTTTCTGTAA	ACACATACCA	TAGAACTTAA
73851	GACAGGCATA	CAAATAAGTC	ATATTTTTCT	TCTTCAAAAA	TCTGGGAATT
73901	CTTTACAAAAG	AAAAGAAAAA	AAAAAAAAAA	CTAAACTCC	TGTCCATGCT
73951	GCTTGTTCTA	GAAAGGGATA	TTGGCACATA	CACACAGCCC	TGCTTTTCCC
74001	ATTCAGGTGA	GACAATATCT	GACAGTGTCT	GCAGCCAAAG	CCCCAGGGGG
74051	AAAAGCTGCA	CGCTTGGTGC	TACCTCTCGG	CCGCCTCATG	CATTACAGGG
74101	ACCTGTGCCT	GTCATTCAGG	CACAAGGTGA	CGGGGCTGCA	CTCTGGCACA
74151	CTCCAGGTGT	TTGTGAGAAA	ACACGGTGCC	CACGGAGCAG	CCCTGTGGGG
74201	AAGAAATGGT	GGCCATGGCT	GGAGGCAAAC	ACAGATCACC	TTGCGAGGGG
74251	CTGACATCAA	GAGCGTAAGT	AGATCCACAA	AGGAGGCAGG	ACCTGGGACG
74301	TTTTCTTTTC	ATAGGAGAAC	TCTGGGATCT	GAATTTGAAG	AAGCCTTGCT
74351	GTGTGAATTC	AGGCTCAGAT	AAAGGTTTGG	GTTTTTTTCT	GGCCTGATG
74401	ACTCCATTCA	GTGTCTCTTT	CTGAAACCAC	TTTCTGCTTC	TTTATCTTTC
74451	TTCATTGCAA	CCTGTGATCA	CCACCTCTCC	CTAACCTTGG	TAAAGATCCA
74501	TTTTTTTTTTA	ATGGAATAAA	AAATCTAGGA	ATAGAAAAGT	TTTTTTGGTT
74551	TTTTTTTAAAG	TTGATCAACA	GAAACTTCCA	AGGGTGGGGT	GGTGAGCTTA
74601	ATTGTTCCCTG	CTTTCCCTTT	CCTTTTAATT	CCTTAGATTT	CAAACCTTTA
74651	CTACCATAAA	TTACCCAGGA	GATGGTCTTT	TTTTCTTTTT	TGAAATGTTT
74701	CTTTCAAGTT	CAAAATTTTT	TCTTTGTTTC	AGAGATCACA	GTTAAGCAGC
74751	GTAGGGTGGG	AACTCAGAAC	TACAATTGGA	AAGCACTATT	CTATTCAGGA
74801	CAGGATGTGG	GAAGTGCTTT	GATGGAATAT	ATAAATTGTA	TCTTAAGTAA
74851	TCAAGACATA	GGTAGCAAAA	AAATGGTCTA	GGGCATCCCA	ACAAAATTAT
74901	GAATGCATTT	GGGAAAATGT	CATCATTTTG	CTGGTGCTTA	TGAAACTTGC
74951	TGTTGGGAGA	TACCTATGCC	TGTATGTAGG	TATAGTTTAT	AAGAAACCAT

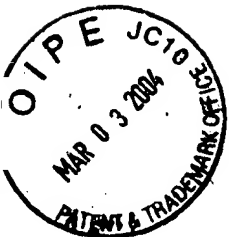
FIGURE 3Y



REPLACEMENT SHEET

75001	TTTAGAAAAGA	AAAGATAGAT	TCCATTAATA	CAGTTTTTAT	CAGAGTACTT
75051	GGATTTTGTT	TAATTCCTAC	ATATTTTTTC	TTAAAACCTT	TCTCAGTATT
75101	TTTATTGTTT	AGAGAAATAA	AACAAGATAA	TCATTTTAAA	TCATAGCACT
75151	TACGTTTTCT	CTTGTTTTAT	AAGGAGCAAG	GATGCTCTAT	AGAAAAATA
75201	ATGTAAGAAT	AATAAAAGTT	TTTGGTTTTT	ACATAGGTAA	AGCAACAGTG
75251	TGATTGGATT	ATGGTGTTTG	ATTCTATTCC	ATTTTCAGCA	AGAAAGCGAT
75301	GTAAACCACA	AAGGAACTAA	GAAACATTTA	AGATAGGCTG	TGTGATTATG
75351	ATCTTTTCAG	TCTTTGGCTC	CTAATATCTG	TTCCTTTATA	TTCTATCACA
75401	CTCTTCTAAC	TTTGGTAATC	CTTGACAAAA	GTGTGCACTT	TATAAACAAAT
75451	CCTAAATCGA	ATTGGTCTAT	AGCTTAGAAT	GGCTTTTTAA	AGAATAATTG
75501	ATTCTGAGTA	ATGTGGTCTG	ATGAACAGTT	TGATGACTTC	AGTTTCTACT
75551	GAAAGAGAAG	CTTCAGTGAT	ACTGGCAACT	ATATTCTGTT	TTTTTCCTCC
75601	TGCAAAATAA	GTTTAAAAAT	GGTTTGGGGG	AAGGTTTGCC	TTTATTTTTG
75651	CCTAATAAGG	AGGCATTAGA	AAGGGGCAGA	GGAGGCTTGA	CTGGTGTGTG
75701	CATTCTCTCC	CTAGGTCGTC	TTCAAAGGTG	AAAAAAGGCG	TGGTCACACT
75751	GGGGAGATTG	GATTAGATGA	TGTGAGCTTG	AAAAAAGGCC	ACTGCTCTGA
75801	AGAACGCTAA	CAACTCCAGA	ACTAACAATG	AACCTCTATG	TTGCTCTATC
75851	CTCTTTTTCC	AATTCTCATC	TTCTCTCCTC	TTCTCCCTTT	TATCAGGCCT
75901	AGGAGAGAG	TGGGTCAGTG	GGTCAGAAGG	AAGTCTATTT	GGTGACCCAG
75951	GTTTTTCTGG	CCTGCTTTTG	TGCAATCCCA	ATGAACAGTG	ATACCCCTCT
76001	TGAAATACAG	GGGCATCGCA	GACACATCAA	AGCCATCTGT	GGGTGTTGCC
76051	TTCCATCCTG	TGTCTCTTTC	AGGAAGGCAT	TCAGCATGCG	TGAGCCATAC
76101	CATCCTCCAT	CCTGATTACA	AGGTGCTCCT	TGTAGCAAAT	TATGAGAGTG
76151	AGTTACGGGA	GCAGTTTTTA	AAAGAAATCT	TTGCAGATGG	CTATGATGTT
76201	ATGTGTTCCG	TGTTGTACCA	TGAGTAGTAT	TGACTTCCCT	TGAGATATGA
76251	TGTACAAATG	GCTTGTGAAA	TTGACTTACC	CTCTTCACTT	AAGTTAGTTC
76301	TGGCCTGACC	TGAACCTCTG	CTTTTACTGC	CATTCACTTT	ATAAAATAAG
76351	GGTGTGTAAC	ATATCAAGAT	ACATTTATTT	TTATCTGTTT	TTTTTTTCCT
76401	GTTAAAGACA	ATTATGTAGA	GTGGGCACGT	AATCCCTCCT	TAGTAGTATT
76451	GTGTTTTGTG	TAAATGTGCT	ATTGATATTA	AGTATTTACA	TGTTCCAAAT
76501	ATTTACAGAC	TCTAGTTGCA	AGGTAAAGGG	CAGCTTGTGA	TCTCAAAAAA
76551	ATACATGGTG	AAATGTCATC	CAGTTCATG	ACCTTATATT	GGCAGCAGTA
76601	GGAAATTGGC	AGAAGTGTTG	GGTTGTGTA	ACGGAGTGAT	GAATTTTTTT
76651	TTAATGGCCT	TGAGTTTGAT	CTCTGCAAAG	GATAGGAAAC	CTTTAGGAAG
76701	ACAAGAACT	GCAGTTAATT	TAGAAGTGTC	ACTGTTTCAA	GTTACACTTT
76751	AAAACACAG	CTTTTACCAT	CATAACATGG	CTCTGTAAT	ATGTAGGAAG
76801	CTTTATAAAA	GTTTTGGTTG	ATTTCAGAAA	AGGATCCTGT	TGCAGAGTGA
76851	GAGGAAGCAT	AGGGGGAAC	TCCATTGGAA	CAGATTTTCA	CACAACGTTT
76901	TAAATTGATA	TAAGTTTAGG	CAGTTGTAGT	TCATAACTTA	TGTTGCTCAT
76951	GTTGTGCTGT	GTCAGGATGG	GATAGGAAGC	AAGTCCCATG	CTTAGAGGCA
77001	TGGGATGTGT	TGGAACGGGA	TTTACACACA	CTGGAGGAGC	AGGGCAAGTT
77051	GGAATTTCAA	GATCCATGAA	CCCCCAACTG	TATTTCTCCT	CTGCATATTT
77101	TACCAATATA	TTAAAAACA	ATGTAACCTT	TAAAAGGCAT	CATTCTGAG
77151	GTTTGTCTTA	ATTTCTGATT	AAGTAATCAG	AATATTTTCT	GCTGTTTTTG
77201	CCAGGAATCA	CAAAGATGAT	TAAAGGGTTG	GAAAAAAGA	TCTATGATGG
77251	AAAATTAAAG	GAAC TGGGAT	TATTGAGCCT	GGAGAAGAGA	AGACTGAGGG
77301	GCAAACCAT	GATGGTTTTT	AAGTATATGA	AGGGTTGGCA	CAGAGAGGGT
77351	GGCGACCAGC	TGTTCTCCAT	ATGCACTAAG	AATAGAACAA	GAGGAACTG
77401	GCTTAGACTA	GAGTATAAGG	GAGCATTCT	TGGCAGGGGC	CATTGTTAGA
77451	ATACTTCATA	AAAAAGAAG	TGTGAAAAATC	TCAGTATCTC	TCTCTCTTTC
77501	TAAAAAATTA	GATAAAAATT	TGTCTATTTA	AGATGGTTAA	AGATGTTCTT
77551	ACCCAAGGAA	AAGTAACAAA	TTATAGAATT	TCCCAAAAGA	TGTTTTGATC
77601	CTACTAGTAG	TATGCAGTGA	AAATCTTTAG	AACTAAATAA	TTTGGACAAG
77651	GCTTAATTTA	GGCATTTCCC	TCTTGACCTC	CTAATGGAGA	GGGATTGAAA
77701	GGGGAAGAGC	CCACCAAATG	CTGAGCTCAC	TGAAATATCT	CTCCCTTATG
77751	GCAATCCTAG	CAGTATTAAA	GAAAAAAGGA	AAC TATTTAT	TCCAAATGAG
77801	AGTATGATGG	ACAGATATTT	TAGTATCTCA	GTAATGTCCT	AGTGTGGCGG
77851	TGGTTTTCAA	TGTTTCTTCA	TGGTAAAGGT	ATAAGCCTTT	CATTTGTTCA
77901	ATGGATGATG	TTTCAGATTT	TTTTTTTTTT	AAGAGATCCT	TCAAGGAACA
77951	CAGTTCAGAG	AGATTTTCAT	CGGGTGCATT	CTCTCTGCTT	CGTGTGTGAC

FIGURE 3Z



REPLACEMENT SHEET

78001 AAGTTATCTT GGCTGCTGAG AAAGAGTGCC CTGCCCCACA CCGGCAGACC
78051 TTTCCCTTCAC CTCATCAGTA TGATTCAGTT TCTCTTATCA ATTGGACTCT
78101 CCCAGGTTCC ACAGAACAGT AATATTTTTT GAACAATAGG TACAATAGAA
78151 GGTCTTCTGT CATTTAACCT GGTAAAGGCA GGGCTGGAGG GGGAAAATAA
78201 ATCATTAAAGC CTTTGAGTAA CGGCAGAATA TATGGCTGTA GATCCATTTT
78251 TAATGGTTCA TTTCCTTTAT GGTCATATAA CTGCACAGCT GAAGATGAAA
78301 GGGGAAAATA AATGAAAATT TTACTTTTCG ATGCCAATGA TACATTGCAC
78351 TAAACTGATG GAAGAAGTTA TCCAAAGTAC TGTATAACAT CTTGTTTATT
78401 ATTTAATGTT TTCTAAAATA AAAAAATGTTA GTGGTTTTC AAATGGCCTA
78451 ATAAAAACAA TTATTTGTAA ATAAAAACAC TGTTAGTAAT ACCAGTTGTC
78501 TATTCTTGTT TTTTGAGTTT TGTTTTTTTT TGACTTGGA AAAAGCATTG
78551 AGGTAGTTAA ATGATGTTTC ACAAAGTCA TAGTAGAATC CCTTTTACTG
78601 TTTGGATGGT GGGAACAAAG ATGTTGCCTG CAGTATTATA CTTTCTAGGT
78651 TATAAACAT GAGACACTTT ATTTTTTTTA TCAGCATGAA CAGGGAAAGA
78701 GATCAGAAGA TCACTATAAC CCATGCCATG CCTTAGTAAA TTGCTTTAGT
78751 TATGTTTAT TATCATTTCA TTGTAAACAT TTGCT (SEQ ID NO:3)

FEATURES:

Genewise results:

Start: 3000
Exon: 3000-3070
Exon: 5248-5348
Exon: 19533-19583
Exon: 34426-34518
Exon: 39701-39790
Exon: 44102-44221
Exon: 45394-45513
Exon: 47168-47302
Exon: 47607-47729
Exon: 49126-49127
Exon: 49132-49522
Exon: 65277-65363
Exon: 65834-65932
Exon: 74008-74264
Exon: 75715-75807
Stop: 75808

CHROMOSOME MAP POSITION:

chromosome 4

ALLELIC VARIANTS (SNPs):

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
3365	C	T	Intron			
3411	G	A	Intron			
5243	G	A	Intron			
6532	T	G	Intron			
9208	-	G	Intron			
15833	T	C	Intron			
27795	G	T	Intron			
31341	A	G	Intron			
33370	G	A	Intron			
37788	G	A	Intron			
41465	C	T	Intron			
41466	A	G	Intron			
41653	T	G	Intron			
47666	G	A	Exon, coding	281	V	I
52613	G	A	Intron			

FIGURE 3AA



REPLACEMENT SHEET

52645	G	A	Intron
59197	-	A	Intron
63508	T	C	Intron
75153	C	G	Intron
76017	C	G	Intron
76033	C	T	Intron
77194	A	G	Intron
77508	T	A	Intron
77557	G	A	Intron

Context:

DNA

Position

3365

CGGGAGGTGAGCTGGGCCCCGGGGCGCCCTCTCCTCCTTCCCGCGCTAATTTACACTCA
CTGTCTTGGGTCACTTTTCCCCGCGGGGTTTCGTGGTCAGAGAGGCGTCTCCTCCATCCA
GAAGTTGGGCCACCGCACAGCGTGGCGCAGGAGAGCGGTCCAGCGGCTCCGAGTGGCCG
CCCGAGGCGGAGAGGGCGCGCCCTTGCGAGTCTGGGACCCATCCGCGGCCCCCGAGGG
CGACTCGCCCCGCTCGGGAATTAGGACTGAGGGAGAGGAGCCGCTGGAGCCTGGGATCT
[C, T]
GGCTCTGAGGGCGCGGTTTAGCCACCTACGCCGAGGTGACGCGCGAAACATCCCTTACCC
GGGAACTCCCGCGCCTGAAGTAGACGGCTCTTCACTGGGGAAGCTTCCAGGCCCGGG
GGGAGGCCCGGGCTCTGCTCAGGGCTCTCGGGGCGCTCACACAGAGAGTGGGTGCGAGT
CAGCGACTGGGCTACGGGGGAGATTTGTGGGCCCTCTCCATTGGTTTTCTTGAGGGAAGG
AGACTCAAAATGAGGACCGGAGGGTGGGCGCTCCGTGAATGTGAGCATGAGTGTGTGGAT

(SEQ ID NO:7)

3411

TAATTTACACTCACTGTCTTGGGTCACTTTTCCCCGCGGGGTTTCGTGGTCAGAGAGGC
GTCTCCTCCATCCAGAAGTTGGGCCACCGCACAGCGTGGCGCAGGAGAGCGGTCCAGCG
GCTCCGAGTGGCCCGCCGAGGCGGAGAGGGCGCGCCCTTGCGAGTCTGGGACCCCATCCG
CGGCCCGGAGGGCGACTCGCCCCGGCTCGGGAATTAGGACTGAGGGAGAGGAGCCGCT
GGAGCCTGGGATCTCGGCTCTGAGGGCGCGGTTTAGCCACCTACGCCGAGGTGACGCGCG
[G, A]
AACATCCCTTACCCGGGAAACTCCCGCGCCTGAAGTAGACGGCTCTTCACTGGGGAAGCT
TCCAGGCCCGCGGGGGAGGCCCGGGCTCTGCTCAGGGCTCTCGGGGCGCTCACACAGA
GAGTGGGTGCGAGTCAGCGACTGGGCTACGGGGGAGATTTGTGGGCCCTCTCCATTGGGT
TTCCTGAGGGAAGGAGACTCAAAATGAGGACCGGAGGGTGGGCGCTCCGTGAATGTGAGC
ATGAGTGTGTGGATGTGTGTGTGAGAGCGCACACACTGCGCCGCTCCTCAGACTCGGGCG

(SEQ ID NO:8)

5243

GGCAGCCTTGAGAATTGTTGGTGTAGCTGGTGTATTTCTACTTAAGAAAGCATCTTTC
CCTCCCGTTTTTTCTCCTACCCCTGTGTGTGGGGGATGGGGTATTTAACTGTCTGAAAT
TTGACATTAGATCATAGCAGAACTATTTCTGTGAAGGTGTTTTAACCTTAAATTTCTGCA
GGCATAAAAGAGTTGTAGAAAATGTTGGGTGTGGTTGACATTTTTCTGAAGTAATAA
TACAGAGGAAATTACCTTTCTCTCAAAAGTGCTCTTATTTATTTGAATCTTTTTTTTT
[G, A]
GTAGGTGGCCAGGCAAATAGTGTATCGATTGGCCTATGTCGTTATGGTGGGAGGATTG
ACTGCTGTCTGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTGACGCTGAGTATCAAGCCT
GGGGACTTCAGTTCCCTGGGAGGTGTGGCTTTCCACCTTGTTTCATGGCTTCACCCACAT
ATCAGAGGGTTTACTTACTGAGCAAGGCTTGGCCTTGACAGTCTGACTTGGGGATTTTCAG
GTACAGTCCAGACTCCTTATTTCTGCTTCTTTTCAGCTTTAGCCACCTGTATTACGGCCCA

(SEQ ID NO:9)

6532

GGGCGGGGTAGGGGCACTTCTGGTAAGATGATGGGAACTAAGTTGGGTCTACATTGG
GATATATATTTTATGCTAATGAGGAGGAGGCTTAGAGGAAGAGAGAAGGGCAGTTACGA
AGGCTAGAGCTGGCAATGGAGAAGCCTGCCTTAGAGATGGGTGCTAGTGTGAGGAGTCA
GGCAAATTTAAGTTCAGGAAAGTTAGGAGTTCCCTCTGCTATTTTAATTTTGGAGATGC
TTGCAATGTCTTCTTAATTTTGTGAAAGAGGACAGTGACAGTCACAGATTGACTCTAA
[T, G]
TGCACATAAAGACCACAATCTCTGGTTGGGAATAGAAAGGTAAAGGAAATGAATGTTTGC
CTACCTGGTATGGAATTTGAGAACCAACAGATTCTAATAACCAAAATGTGAAGAAAGGAC
CCTTCTGTTGGCCCAACACACCTACACATAACCCCTCTGAGTGAAAAATGAGTAGTTCTA
TACCTGCAGTCTCCAGCTGTGCAAATACTTCTGATACTACAGAAGACTAAATTCACCCAG

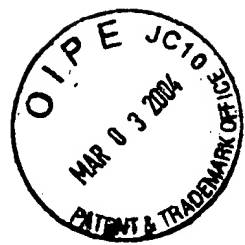
FIGURE 3BB



REPLACEMENT SHEET

- GCACCATTCTTCTTTTTTGATCATCTTCCCTTAAACAATATTGAATAGACTAACCAGTG (SEQ ID NO:10)
- 9208 TCTGAGTTCCTTTGGCTGTCATTGAGCAACTTGTGGTTTCTGAAGGAAATTATGTGAATTA
GGATGGTTTTGTATCATTTATCCTTAAGAACAGGGAAAATTGAGATGTTTTCTTATGTTT
CTGCTGGAGATTTTGAAAGATGTGAAACCTACACCTACAGATTGACCTTGCTTAGTTAG
CTCTGAACCTCCTGCTGCCTCTTCCACGTAAAGTGAAAATTTTGGATTCTTATCGGCTTC
AGATAAACTTACAGGTTAGTGAACATAGGGACTGAGATATAGTAATTCATTCTGAAGCT
[- , G]
TTTTGGAGTGGTCAAATAATTTTAGTTGGATAATATATATTACTGGCTAATGATTGTGGA
TATTGGAAGTGATGAAAAAATTATTGAATTATTTCTTTCTGCATTTCAAATGAAAAGGCT
ATTAGTTTGAGCAGAGAATTTTGATTTAGTAAACAAAATATTTAAATTTTCATGTTTCATT
TCTTTCTCCTATCTGGGTTTCAGATACTCAGTCTTATAAATGGAACATGATTTATTTTTC
TCCCTAAACTGGTTATTAACTTCCGTCCATAATCACAAAACATATATAGATTATATATTT (SEQ ID NO:11)
- 15833 CATACATTAGCTTTGGTAGATACTAGATGCCAGGGGAGTGCAAATTTGAGAATAAGGATT
TGGCATGGGTTATTGTCATGTTGAGAGTCAAGATTTAACTAAATTTTAAAACCAAACACT
TCATTTGATCAATATCTTTTAAACCATTCTGTAGATTAATAATATAAATTCTCCAGAGCT
GACATTACTTTGCTATAACATCATCAGATCACAAGATTAGGGTTGCCTTTTGTAGATGTT
ATTCACTTACTCTGAAATGTTAGGAAATATGTCATCACAGTTTAAATTTGTAGTAATATA
[T, C]
ACAAAAGGAAAACACAACCTAGGAATTTTGGATTATGCTTACTTTGCCAAAACCATGTT
GATTTTCAAAAACCTTTAGCC (SEQ ID NO:12)
- 27795 ATGAAAACAGAAAGAGAAAGTTAAAATTTCAAGTAACTGAAAACAACAATAGTGCTCAG
AGGATTTTTTTTTTAAGTGAAAAGGGATAGTGCTTAATTATGACAAATAAAAGCTAACTTG
AGATGCACATATACAGATGCAGCCACTTATTTTGGCGGGGACACTTCAGGAATTAATAA
TTAAATAGCGAGAGATCAAATAGATACTTGGTAAATGTGTCTGAATTGGATGTTCCCGA
CACAAAATAAAATGAGTTATTGACAGCTCTTGGGAGACAACATTATAAAGACTAGACAC
[G, T]
TTATTTATTTTAACTCTATGTTCTAAATTACCATTGAGTAATTGACATTCGTATTTGACT
ATGGTTTGTGGTTAAGTTCTTAATTGCAATAATGTAAATAAAATGTGAAGCCCAAAGCA
AACAAACAACAAAATATAGCAATACTTCAACAGAGGTAATAATAATATGCTGCATCAAT
GGTTCAGAATCCAGCATCTACATAAAACAAGCAACAGGGTAATGAAATATTTTCTTTTC
AAATATTCTGGCAGAGCTACTTTAGTTTTCTTAAGTTATAGATTGTGGTCTTAACGCAA (SEQ ID NO:13)
- 31341 CCACTTTGCTTATATTCTGAAAGTCTTTTGTTCCTATTCCACTGCTCTTACCTCTAACA
CACTGCCTCTAACACACCAACCTGCAGTTGTAGTTATTACACACCCCTCCTTGGTTCTTTC
ATCTCTCTATCACAGCCCTTGTGTGGTTTAGCCAATATATTTTAGTCCACAGCTAAAT
TTTCATACCCCTCTAGACTCTCTAATCCCCTGCCACACTTGCCCTACTATAATACATTATA
TATATAACAAATGTTTGATACGTATTTATTGAATTCCATTCCAGAACTAATGCCAGCAAG
[A, G]
TAACTTTGTGCTATATAGGAGAATATCTTTTGTGCAACAGTTTCAAAGGGTTTTCTTT
TTCTAAGAAGAAAGAAATTGATTGTATCAACTTTATGAGTATCCTACCGCATTTAATAGC
CATTGGCTAATCTAAGGGTTCCGTGGTACTTCACTGAATAGCCTATCAGATGGAAGTGCA
AACACAGTTTGTTTTGAAATAGGACTCCCTAAACATGGAAGAAACATTAACAGTGTGG
CCTGTTGGAATGTGTGCATTTGATGTGCTCAAGATTAGGGCACTTGCTTGAGAACAAT (SEQ ID NO:14)
- 33370 CCACTCACCTGATTGTTTCTCACTCTTCCCTCCACCATTTACCCATCTCTTTAGCTTAATG
AGTCCCCTGTGTATCTCCCACTAAACAGCGGCTTACTTGCCCTGTGAAATATTCTTCTCT
TGGGTAGTCTGCTCCCTTCTCTGTCTACTCATGCTTCAAGATTCAACATAAGCCTCTCT
ATGAGGCTTTCTGCACGTATGTATATGGATTTGCTTGTGTAATGATTCTTTCACAGATTT
CATATTGCTGATAAATAAATATTGTTTGAATAAGAAACGTGGTTTGTATTTTTATCTC
[G, A]
ATTGTAGACTCCCTTGAGACCAGTACCATGCTATACAATTATTTTTCATCTATTATAGTGT
CTGGCATAGGGACATGCACATATTTGGTACAGAA (SEQ ID NO:15)
- 37788 GCCCTGTCAGGATCAGGGAAGCTGCCATGTGTGGCTGGTTGAGTGTGAGAGCTGCCTAG
AGACTTCCATAAAAGTTGTTAGAGAAAATTGTTGATAGTGCTTACATAGCAGATTAACTT
AAACTGTTTTTCATTACAGGCCACACATTTTAATAAAGTAGAAAATATGCTTTCACAGATAA
GGGAAATCAAACAGGCTCCTTTTTTCTGGAGGAGAGAAATGTCAAAAAGAATTAAATTTG

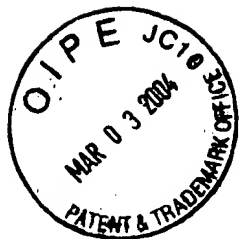
FIGURE 3CC



REPLACEMENT SHEET

- AAATAACTTTACAGAACTGGAAATTAGCTTTTGATTAAAAGTAGCTTTTGGTATATGACA
[G, A]
GTATTTACTGAGAATTTTGTAGCGAGTTATATACTTTAAGAAATAACCCCGAGAACTTG
CATCATGGTGTAAACAGCTTGAATAAACAAGTGCCTAACAGTGCCTTTAGAGCTGCCTG
GGAAACAGCCAGAATACCAGGGCAAGCTGCATTTTGGAACTGGTTAATTTAGTAGCCTT
GCCACAGGCTTAGTGTGATCTGCTTTTGGTGGCTTGATCTTCCCCACTAAGTCATTTTCT
GGATTTGTTACACCTAGAACTGTTAGGAAATTACAGGCTTGGGCTGATCATTAACATACT (SEQ ID NO:16)
- 41465 TTTATTTCTAGGTTCTTTTATCAACTTTTAAAGATTTATTTGAGACAGTATGATCAATGAC
TTCATTTTGTCTGCTTATTATTGTAGGAGTATTTACTATAATTTGGAAGTAATTTATTT
TTGAATTTATTGCTTAATTGAATGATCTCCAATAGATTGTGATAATGAACACAGCATTTA
TAGAAAGCAGCACATATTAACTTACTTAATATGGCACTAGGTCAATGAGAAAAGAAGGTA
ACATAATTGAAGACAAGAACTCTTAAGAAAACCTGAGGACAAAAAGGCTTCTCACCAGGA
[C, T]
ACCAGATGCATTTAATCTTTTGAAGCTCTGTACTTTAGGAAAAGCTGATATTTGGCAAA
TTTGTATAAACATGGATGACTATGGAATCCTATTTTATAGTATCTGAAGTGGCTTTCATA
AGGGTCATTGTGAAGTTTGTAGGAGACACCTGCCTGTGGCAGATGGGACAATGATGGCAG
TCACTAGTGATATTAACACCAGTCAGCTGTGAGGAATATCATCCAGACCATCAGCAGCT
GGTAGAGTACAGCTTTCTCAATTGCTTTCCATGTTTGGATACCTATATGCCCCGTTAATA (SEQ ID NO:17)
- 41466 TTTATTTCTAGGTTCTTTTATCAACTTTTAAAGATTTATTTGAGACAGTATGATCAATGACT
TCATTTTGTCTGCTTATTATTGTAGGAGTATTTACTATAATTTGGAAGTAATTTATTTT
TGAATTTATTGCTTAATTGAATGATCTCCAATAGATTGTGATAATGAACACAGCATTTAT
AGAAAGCAGCACATATTAACTTACTTAATATGGCACTAGGTCAATGAGAAAAGAAGGTA
CATAATTGAAGACAAGAACTCTTAAGAAAACCTGAGGACAAAAAGGCTTCTCACCAGGAC
[A, G]
CCAGATGCATTTAATCTTTTGAAGCTCTGTACTTTAGGAAAAGCTGATATTTGGCAAA
TTTGTATAAACATGGATGACTATGGAATCCTATTTTATAGTATCTGAAGTGGCTTTCATA
GGGTCAATTGTGAAGTTTGTAGGAGACACCTGCCTGTGGCAGATGGGACAATGATGGCAGT
CACTAGTGATATTAACACCAGTCAGCTGTGAGGAATATCATCCAGACCATCAGCAGCTG
GTAGAGTACAGCTTTCTCAATTGCTTTCCATGTTTGGATACCTATATGCCCCGTTAATA (SEQ ID NO:18)
- 41653 AGCACATATTAACCTACTTAATATGGCACTAGGTCAATGAGAAAAGAAGGTAACATAATT
GAAGACAAGAACTCTTAAGAAAACCTGAGGACAAAAAGGCTTCTCACCAGGACACCAGAT
GCATTTAATCTTTTGAAGCTCTGTACTTTAGGAAAAGCTGATATTTGGCAAAATTTGAT
AAACATGGATGACTATGGAATCCTATTTTATAGTATCTGAAGTGGCTTTCATAAGGGTCA
TTGTGAAGTTTGTAGGAGACACCTGCCTGTGGCAGATGGGACAATGATGGCAGTCACTAG
[T, G]
GATATTAACACCAGTCAGCTGTGAGGAATATCATCCAGACCATCAGCAGCTGGTAGAGT
ACAGCTTTCTCAATTGCTTTCCATGTTTGGATACCTATATGCCCCGTTAATAACAGGTAA
AATAGCCAGTACATCATTTCCACATTTACCCATTGAATGTTGCATGTTTCTTCTCTTCA
CATATTCATACAGTCCAGATTTTGTGGACTCATGACGACATTTGGCTTTTCTTTCTCC
TTTCAGTTTCATGATTCTTAACCCCAAAGTGTCTTTGCCATGGGAACGGAAGGATAAATT (SEQ ID NO:19)
- 47666 GTGGTGATGGCTGGAATGTGAGGGGAGGGGAGAGTACTGGCGTTAAGTTAAACCAACAG
ACATCCAGTTTAAACCACTGGTAGTTCTCAGTCTACATGTAGTTTATTTCTTCTGTTTATC
TGCCAATTTTATGTAGATCATCACATTTGCCAAAAAATCATTTTGTAACTGTATATAT
TTTTTATGTCATCATATTTATCTCCTAAATAAGTCTCTTCTTTTCTTCTACTTTCTGATGCA
GACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAAC
[G, A]
TACGTGGGTCTTACAAGTGCAATGTAAAGAAGGATACCAGGGTGTGACTGACTTGTG
TGTGTGAGTAGCACTTGTCTCTCAGCTTTAAATTTAGCAGGAAATACAGGATTACACAA
AGGCCATTGCTAGGGAATAAGGAATAAGATTATCAAGAAGTATAATTGTCATAATTG
GTTATATTTGCTTTGATTTCCACAAACAATAAAATCACTTGTCTCAGGTACTTGTAAAAA
CTAAGGACTCAGTAATACACTATAATCTTAAGAGTATTTAATCTCTTCACTGAAATCTC (SEQ ID NO:20)
- 52613 AGGTAATGGGACCTCTATCACCTGTTGCTAAGGTCTAATAATGTGGATTTCATCCTTAATT
ACTCTTCATACATACAGTCAATATGTAAGGAAATCCTGTAGCTGTACCTTCAAATTATA
TTTAAGTGTGACCTTTTCTCACCACCTCCAGTGTACACCCCTGGCCCAAGCCATCTCTC
CCCTGGAATACAGGCCCAAAATCCTTTATCCAATAACTTATGGAATATAGCATTTTATA

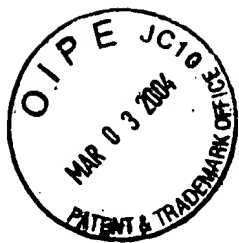
FIGURE 3DD



REPLACEMENT SHEET

- GATTTTAGAAAAATCAGTAAGGTACACATACTATATAGTACACACTGAAGTAGTGAAACAT
[G, A]
CTGATTTTCCTCTAGTGCCTTTACTGTGAACGTATCAATGTTAAGGAAAGGAAAAATGATA
TTAACTCAGAGATGATGTCTCACAGCATATATTTACTAGCTTGACACAAATTTTTTAATGT
TAGCAAGATTTAAGGCAAATTTTTACTTATATTTAATTGGATCCTATGATGATTATTA
AAGAAAAAAGTAGTTATCTCTAGAAAGTATAAATTGAGCTCTGGCAAATGTGAGCAAAA
CCAGAAATCAGATTTTTTTAAAGTTACGTGTACATTTGTCTATAGAGTTATAATTTAAAG (SEQ ID NO:21)
- 52645 GTCTAATAATGTGGATTTCATCCTTAATTACTCTTCATACATACAGTCAATATGTAAGGAA
ATCCTGTTAGCTGTACCTTCAAATTATATTTAAGTGTGACCTTTTCTCACCAACTCCAGT
GCTACCACCTTGGCCCAAGCCATCTCTCCCTGGAATACAGGCCCAAAATCCTTTATCCA
AATAACTTATGGAATATAGCATTTTTTAGATTTTAGAAAATCAGTAAGGTACACATACTA
TATAGTACACACTGAAGTAGTGAAACATGCTGATTTTCCTCTAGTGCCTTTACTGTGAAC
[G, A]
TATCAATGTTAAGGAAAGGAAAAATGATATTAACCTCAGAGATGATGTCTCACAGCATATAT
TTACTAGCTTGACACAAATTTTTTAATGTTAGCAAGATTTAAGGCAAATTTTTTACTTATA
TTTTAATTGGATCCTATGATGATTATTAAGAAAAAAGTAGTTATCTCTAGAAAGTATAA
ATTGAGCTCTTGGCAAATGTGAGCAAAACCAGAAATCAGATTTTTTTAAAGTTACGTGTA
CATTTGTCTATAGAGTTATAATTAAAGTATTGTGCTCATAGCCAGTCTGTGATCTGGGG (SEQ ID NO:22)
- 59197 CTACTATTGATGTTGAATTCATTTATATAGTAATGATAACATTTCTACTTAATTCATAA
AAAGACAGCCTATGCTGTTTTCTTGTCTGAGTTTATATGTTTCTCATGCTTTTTATTAT
GGTTCATTACAAATTTTAATGTTATTTTTAACTAACTAGATCCTTTTGAAACAAATTGGTT
TGCAAGTGTGAGCTGTTAGGTGCACAGAGAAAAATGAAAATAGAACTTGGCATTTTTATT
CTAGGCTTGTACCAATATTTAGAATACTGTGTTTTATTAGGTGTTTAGTCTCATT
[-, A]
GACAGTTGTGATTTTTAAATAGAGACCACATCATCTCAACTTCTTTACTGTGAAAATAAT
GACAATAGTCTTTTCAGAGATGAATCTGTCTAGATGGGAAATTACATGATTGATCTGAT
GAGNN
AAAAATACTGACAAGTAGTTCCCCAGAAAATCTGATTTAGTAAATGTACCAAAAGGAT
TTAGAAATCTACATCATAAATAAACATTCTATGTTATTTTAGTTCAGACCTATTTTAAT (SEQ ID NO:23)
- 63508 ACAGGCTCCCGGTGCCAGGAAACCTTTACATCAACACTCGATTTGCCATTTGATAGTCCT
TCATCTGGGAGGAAAAAAGACGGAGGGGAGCTTGAAAACTGTCTATAATGTCCCTGG
AATATGGTACTTTAAGAGTTGAGCCTATTCCATTTGGAGATGATTATATAAGTTACA
ACAAAAGAAGGGGACAAAAACATGATTGTTCTATGGAGTTTTTATAACTTTCTGTCAAA
GAAAGCACGCTTGTCTACAATTTTGTAATATTTCTAGTAAATAAAAGAGGCACTCCCGT
[T, C]
TCAGAGCACCAATAAGGAAAGTGAATTGGATGTCATTGCTGTGTCAGTCAGCTGGGCTAT
AAAAGAGAGAGTGGGGTTGCCATCCCTGGGTATCCACAGTCAGCTGTGTCCCTAGAG
CTTCTTTTCTTTCATTGCTGCCAGCTGGGTATATTGCAAGTATGGATTATAAGAGGGGA
AGGGAGTCACTGTTTTAAGCTTTGAAACAAAAGGAAAAAATCAGAAGTAGTAAGCTA
AAAACAACTTGTGCAACGTTCTGGGATTATTACTTAATTTTAAAGATTTTGTCTAAAAA (SEQ ID NO:24)
- 75153 AAGACATAGGTAGCAAAAAATGGTCTAGGGCATCCCAACAAAATTATGAATGCATTTGG
GAAAATGTCATCATTTTGTCTGGTGCTTATGAACTTGCTGTTGGGAGATACCTATGCCTG
TATGTAGGTATAGTTTATAAGAAACCATTTTAGAAAGAAAAGATAGATTCCATTAATACA
GTTTTTATCAGAGTACTTGGATTTGTGTTAATCTTACATATTTTTTCTTAAACTTTTC
TCAGTATTTTTATTGTTTAGAGAAATAAAACAAGATAATCATTTTAAATCATAGCACTTA
[C, G]
GTTTTCTCTTGTTTTATAAGGAGCAAGGATGCTCTATAGAAAATATAATGTAAGAATAAT
AAAAGTTTTTGGTTTTTACATAGGTAAAGCAACAGTGTGATTGGATTATGGTGTGATT
CTATTCCATTTTCAGCAAGAAAGCGATGTTAACCACAAAGGAACTAAGAAACATTTAAGA
TAGGCTGTGTGATTATGATCTTTCAGATCTTTGGCTCCTAATATCTGTTCCCTTTATATTC
TATCACACTCTTCAACTTTGGTAATCCTTGACAAAAGTGTGCACTTTATAAACAATCCT (SEQ ID NO:25)
- 76017 CGTCTTCAAAGGTGAAAAAAGCGTGCTCACACTGGGAGATTGGATTAGATGATGTGAG
CTTGAAAAAAGGCCACTGCTCTGAAGAACGCTAACAACTCCAGAACTAACAAATGAACCTC
TATGTTGCTCTATCCTCTTTTTCCAATTCTCATCTTCTCTCCTCTTCTCCCTTTTATCAG
GCCTAGGACCAAGAGTGGGTGAGTGGGTCAGAAGGAAGTCTATTTGGTGACCCAGGTTTTT

FIGURE 3EE



REPLACEMENT SHEET

- CTGGCCTGCTTTTGTGCAATCCCAATGAACAGTGATACCCTCCTTGAAATACAGGGGCAT
[C, G]
GCAGACACATCAAAGCCATCTGTGGGTGTTGCCCTCCATCCTGTGTCTCTTTTCAGGAAGG
CATTAGCATGCGTGAGCCATACCATCCTCCATCTGATTACAAGGTGCTCCTTGATGCA
AATTATGAGAGTGAGTTACGGGAGCAGTTTTTAAAAGAAATCTTTCAGATGGCTATGAT
GTTATGTGTTTCGGTGTGTACCATGAGTAGTATTGACTTCCCTTGAGATATGATGTACAA
TGTGCTTGTGAAATTGACTTACCCCTTCACTTAAGTTAGTTCTGGCCTGACCTGAACCTC
(SEQ ID NO:26)
- 76033 AAAAGGCGTGGTCACACTGGGGAGATTGGATTAGATGATGTGAGCTTGAAAAAGGCCAC
TGCTCTGAAGAACGCTAACAACCTCCAGAATAACAATGAACCTCTATGTTGCTCTATCCT
CTTTTCCAAATCTCATCTTCTCTCCTCTTCTCCCTTTTATCAGGCCTAGGAGAAGAGTG
GGTCAGTGGGTGAGAAGGAAGTCTATTTGGTGACCCAGGTTTTTCTGGCCTGCTTTGTG
CAATCCCAATGAACAGTGATACCCTCCTTGAAATACAGGGGCATCGCAGACACATCAAAG
[C, T]
CATCTGTGGGTGTTGCCCTCCATCCTGTGTCTCTTTCAGGAAGGCATTCAGCATGCGTGA
GCCATACCATCCTCCATCCTGATTACAAGGTGCTCCTTGAGCAAATTATGAGAGTGAGT
TACGGGAGCAGTTTTTAAAAGAAATCTTTCAGATGGCTATGATGTTATGTGTTTCGGTGT
TGTACCATGAGTAGTATTGACTTCCCTTGAGATATGATGTACAATGTGCTTGTGAAATTG
ACTTACCCTCTTCACTTAAGTTAGTTCTGGCCTGACCTGAACCTGACTTTTACTGCCAT
(SEQ ID NO:27)
- 77194 AACGTTTTAAATTGATATAAGTTTAGGCAGTTGTAGTTCATAACTTATGTTGCTCATGTT
GTGCTGTGTGAGGATGGGATAGGAAGCAAGTCCCATGCTTAGAGGCATGGGATGTGTGG
AACGGGATTTACACACACTGGAGGAGCAGGGCAAGTTGGAATCTAAGATCCATGAACCC
CCAATGATTTCTCCTCCCTGCATATTTACCAATATATTAATAAACAATGTAACTTTTAA
AAGGCATCATCTCTGAGGTTTGTCTTAATTTCTGATTAAGTAATCAGAATATTTTCTGCT
[A, G]
TTTTTGCCAGGAATCACAAAGATGATTAAAGGGTTGAAAAAAGATCTATGATGGAAAA
TTAAAGGAATGGGATTATTGAGCCTGGAGAAGAGAAGACTGAGGGGCAAACCATTGATG
GTTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTGTTCTCCATATGC
ACTAAGAATAGAACAAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGC
AGGGGCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTC
(SEQ ID NO:28)
- 77508 TCACAAAGATGATTAAAGGGTTGAAAAAAGATCTATGATGGAAAATTAAAGGAACTGG
GATTATTGAGCCTGGAGAAGAGAAGACTGAGGGGCAAACCATTGATGGTTTTCAAGTATA
TGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTGTTCTCCATATGCACATAAGAAAGAA
CAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGGGGCCATTGTT
AGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTTCTAAAAAA
[T, A]
TAGATAAAAAATTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACA
AATTATAGAATTTCCCAAAAGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAAATCTTT
AGAACTAAATAATTGGACAAGGCTTAATTTAGGCATTTCCTCTTGACCTCCTAATGGA
GAGGGATTGAAAGGGGAAGAGCCCAACAAATGCTGAGCTCACTGAAATATCTCTCCCTTA
TGGAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGAT
(SEQ ID NO:29)
- 77557 AAAGGAACTGGGATTATTGAGCCTGGAGAAGAGAAGACTGAGGGGCAAACCATTGATGGT
TTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTGTTCTCCATATGCAC
TAAGAATAGAACAAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAG
GGGCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTC
TTTCTAAAAAATTAGATAAAAAATTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAA
[G, A]
GAAAAGTAACAAATTATAGAATTTCCCAAAAGATGTTTTGATCCTACTAGTAGTATGCAG
TGAAAATCTTTAGAACTAAATAATTGGACAAGGCTTAATTTAGGCATTTCCTCTTGAC
CTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCAACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAAT
GAGAGTATGATGGACAGATATTTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGTTT
(SEQ ID NO:30)

FIGURE 3FF